


SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 
- (i) APPLICANT: Ihle, James N.
Silvennoinen, Ollie
Witthuhn, Bruce A.
- (ii) TITLE OF INVENTION: Jak Kinases and Regulatory Cytokine Signal Transduction
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox
(B) STREET: 1100 New York Avenue, Suite 600
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/665,574
(B) FILING DATE: 18-JUN-1996
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/282,012
(B) FILING DATE: 29-JUL-1994
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/097,997
(B) FILING DATE: 29-JUL-1993
- (ix) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/118,968
(B) FILING DATE: 09-SEP-1993
- (x) ATTORNEY/AGENT INFORMATION:
(A) NAME: Bugaisky, Lawrence B.
(B) REGISTRATION NUMBER: 35,086
(C) REFERENCE/DOCKET NUMBER: 0656.0370002/SLF/LBB
- (xi) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202) 371-2600
(B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Ser Xaa Trp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Leu Pro Gln Asp Lys Glu Tyr Tyr Lys Val Lys Glu Pro Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Ile Glu Thr Asp Lys Glu Tyr Tyr Thr Val Lys Asp Asp Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Val Pro Glu Gly His Glu Tyr Tyr Arg Val Arg Glu Asp Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Ser Gln Arg Lys Leu Gln Phe Tyr Glu Asp Lys His Gln Leu Pro
1 5 10 15

Ala Pro Lys

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Leu Ile Glu Lys Glu Arg Phe Tyr Glu Ser Arg Cys Arg Pro Val
 1 5 10 15

Thr Pro Ser

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Pro Ser Glu Lys Glu His Phe Tyr Gln Arg Gln His Arg Leu Pro
 1 5 10 15

Glu Pro Ser

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3629 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 94..3480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGGGGAACA AGATGTGAAC TGTTTTCCCT CCCAGAAGA AGAGGCCCTT TTTTCCCTC	60
CCGCGAAGGC CAATGTTCTG AAAAAAGCTC TAG ATG GGA ATG GCC TGC CTT ACA	114
Met Gly Met Ala Cys Leu Thr	
1 5	
ATG ACA GAA ATG GAG GCA ACC TCC ACA TCT CCT GTA CAT CAG AAT GGT	162
Met Thr Glu Met Glu Ala Thr Ser Thr Ser Pro Val His Gln Asn Gly	
10 15 20	
GAT ATT CCT GGA AGT GCT AAT TCT GTG AAG CAG ATA GAG CCA GTC CTT	210
Asp Ile Pro Gly Ser Ala Asn Ser Val Lys Gln Ile Glu Pro Val Leu	

25	30	35	
CAA GTG TAT CTG TAC CAT TCT CTT GGG CAA GCT GAA GGA GAG TAT CTG Gln Val Tyr Leu Tyr His Ser Leu Gly Gln Ala Glu Gly Glu Tyr Leu 40 45 50 55	258		
AAG TTT CCA AGT GGA GAG TAT GTT GCA GAA GAA ATT TGT GTG GCT GCT Lys Phe Pro Ser Gly Glu Tyr Val Ala Glu Glu Ile Cys Val Ala Ala 60 65 70	306		
TCT AAA GCT TGT GGT ATT ACG CCT GTG TAT CAT AAT ATG TTT GCG TTA Ser Lys Ala Cys Gly Ile Thr Pro Val Tyr His Asn Met Phe Ala Leu 75 80 85	354		
ATG AGT GAA ACC GAA AGG ATC TGG TAC CCA CCC AAT CAT GTC TTC CAC Met Ser Glu Thr Glu Arg Ile Trp Tyr Pro Pro Asn His Val Phe His 90 95 100	402		
ATA GAC GAG TCA ACC AGG CAT GAC ATA CTC TAC AGG ATA AGG TTC TAC Ile Asp Glu Ser Thr Arg His Asp Ile Leu Tyr Arg Ile Arg Phe Tyr 105 110 115	450		
TTC CCT CAT TGG TAC TGT AGT GGC AGC AGC AGA ACC TAC AGA TAC GGA Phe Pro His Trp Tyr Cys Ser Gly Ser Ser Arg Thr Tyr Arg Tyr Gly 120 125 130 135	498		
GTG TCC CGT GGG GCT GAA GCT CCT CTG CTT GAT GAC TTT GTC ATG TCT Val Ser Arg Gly Ala Glu Ala Pro Leu Leu Asp Asp Phe Val Met Ser 140 145 150	546		
TAC CTT TTT GCT CAG TGG CGG CAT GAT TTT GTT CAC GGA TGG ATA AAA Tyr Leu Phe Ala Gln Trp Arg His Asp Phe Val His Gly Trp Ile Lys 155 160 165	594		
GTA CCT GTG ACT CAT GAA ACT CAG GAA GAG TGT CTT GGG ATG GCG GTG Val Pro Val Thr His Glu Thr Gln Glu Glu Cys Leu Gly Met Ala Val 170 175 180	642		
TTA GAC ATG ATG AGA ATA GCT AAG GAG AAA GAC CAG ACT CCA CTG GCT Leu Asp Met Met Arg Ile Ala Lys Glu Lys Asp Gln Thr Pro Leu Ala 185 190 195	690		
GTC TAT AAC TCT GTC AGC TAC AAG ACA TTC TTA CCA AAG TGC GTT CGA Val Tyr Asn Ser Val Ser Tyr Lys Thr Phe Leu Pro Lys Cys Val Arg 200 205 210 215	738		
GCG AAG ATC CAA GAC TAT CAC ATT TTA ACC CGG AAG CGA ATC AGG TAC Ala Lys Ile Gln Asp Tyr His Ile Leu Thr Arg Lys Arg Ile Arg Tyr 220 225 230	786		
AGA TTT CGC AGA TTC ATT CAG CAA TTC AGT CAA TGT AAA GCC ACT GCC Arg Phe Arg Arg Phe Ile Gln Gln Phe Ser Gln Cys Lys Ala Thr Ala 235 240 245	834		
AGG AAC CTA AAA CTT AAG TAT CTT ATA AAC CTG GAA ACC CTG CAG TCT Arg Asn Leu Lys Leu Lys Tyr Leu Ile Asn Leu Glu Thr Leu Gln Ser 250 255 260	882		
GCC TTC TAC ACA GAA CAG TTT GAA GTA AAA GAA TCT GCA AGA GGT CCT Ala Phe Tyr Thr Glu Gln Phe Glu Val Lys Glu Ser Ala Arg Gly Pro 265 270 275	930		

TCA GGT GAG GAG ATT TTT GCA ACC ATT ATA ATA ACT GGA AAC GGT GGA Ser Gly Glu Glu Ile Phe Ala Thr Ile Ile Ile Thr Gly Asn Gly Gly 280 285 290 295	978
ATT CAG TGG TCA AGA GGG AAA CAT AAG GAA AGT GAG ACA CTG ACA GAA Ile Gln Trp Ser Arg Gly Lys His Lys Glu Ser Glu Thr Leu Thr Glu 300 305 310	1026
CAG GAC GTA CAG TTA TAT TGT GAT TTC CCT GAT ATT ATT GAT GTC AGT Gln Asp Val Gln Leu Tyr Cys Asp Phe Pro Asp Ile Ile Asp Val Ser 315 320 325	1074
ATT AAG CAA GCA AAC CAG GAA TGC TCA AAT GAA AGT AGA ATT GTA ACT Ile Lys Gln Ala Asn Gln Glu Cys Ser Asn Glu Ser Arg Ile Val Thr 330 335 340	1122
GTC CAT AAA CAA GAT GGT AAA GTT TTG GAG ATA GAA CTT AGC TCA TTA Val His Lys Gln Asp Gly Lys Val Leu Glu Ile Glu Leu Ser Ser Leu 345 350 355	1170
AAA GAA GCC TTG TCA TTC GTG TCA TTA ATT GAC GGG TAT TAC AGA CTA Lys Glu Ala Leu Ser Phe Val Ser Leu Ile Asp Gly Tyr Tyr Arg Leu 360 365 370 375	1218
ACT GCG GAT GCG CAC CAT TAC CTC TGC AAA GAG GTG GCT CCC CCA GCT Thr Ala Asp Ala His His Tyr Leu Cys Lys Glu Val Ala Pro Pro Ala 380 385 390	1266
GTG CTC GAG AAC ATA CAC AGC AAC TGC CAC GGC CCA ATA TCA ATG GAT Val Leu Glu Asn Ile His Ser Asn Cys His Gly Pro Ile Ser Met Asp 395 400 405	1314
TTT GCC ATT AGC AAA CTA AAG AAG GCG GGT AAC CAG ACT GGA CTA TAT Phe Ala Ile Ser Lys Leu Lys Lys Ala Gly Asn Gln Thr Gly Leu Tyr 410 415 420	1362
GTG CTA CGA TGC AGC CCT AAG GAC TTC AAC AAA TAC TTT CTG ACC TTT Val Leu Arg Cys Ser Pro Lys Asp Phe Asn Lys Tyr Phe Leu Thr Phe 425 430 435	1410
GCT GTT GAG CGA GAA AAT GTC ATT GAA TAT AAA CAC TGT TTG ATT ACG Ala Val Glu Arg Glu Asn Val Ile Glu Tyr Lys His Cys Leu Ile Thr 440 445 450 455	1458
AAG AAT GAG AAT GGA GAA TAC AAC CTC AGC GGG ACT AAG AGG AAC TTC Lys Asn Glu Asn Gly Glu Tyr Asn Leu Ser Gly Thr Lys Arg Asn Phe 460 465 470	1506
AGT AAC CTT AAG GAC CTT TTG AAT TGC TAC CAG ATG GAA ACT GTG CGC Ser Asn Leu Lys Asp Leu Leu Asn Cys Tyr Gln Met Glu Thr Val Arg 475 480 485	1554
TCA GAC AGT ATC ATC TTC CAG TTT ACC AAA TGC TGC CCC CCA AAG CCA Ser Asp Ser Ile Ile Phe Gln Phe Thr Lys Cys Cys Pro Pro Lys Pro 490 495 500	1602
AAA GAT AAA TCA AAC CTT CTC GTC TTC AGA ACA AAT GGT ATT TCT GAT Lys Asp Lys Ser Asn Leu Leu Val Phe Arg Thr Asn Gly Ile Ser Asp 505 510 515	1650
GTT CAG ATC TCA CCA ACA TTA CAG AGG CAT AAT AAT GTG AAT CAA ATG Val Gln Ile Ser Pro Thr Leu Gln Arg His Asn Asn Val Asn Gln Met	1698

520		525		530		535	
GTG TTT CAC AAA ATC AGG AAT GAA GAT TTA ATA TTT AAT GAA AGT CTT							1746
Val Phe His Lys Ile Arg Asn Glu Asp Leu Ile Phe Asn Glu Ser Leu							
		540		545		550	
GGC CAA GGT ACT TTT ACA AAA ATT TTT AAA GGT GTA AGA AGA GAA GTT							1794
Gly Gln Gly Thr Phe Thr Lys Ile Phe Lys Gly Val Arg Arg Glu Val							
		555		560		565	
GGA GAT TAT GGT CAA CTG CAC AAA ACG GAA GTT CTT TTG AAA GTC CTA							1842
Gly Asp Tyr Gly Gln Leu His Lys Thr Glu Val Leu Leu Lys Val Leu							
		570		575		580	
GAT AAA GCA CAT AGG AAC TAT TCA GAG TCT TTC TTC GAA GCA GCA AGC							1890
Asp Lys Ala His Arg Asn Tyr Ser Glu Ser Phe Phe Glu Ala Ala Ser							
		585		590		595	
ATG ATG AGT CAG CTT TCT CAC AAG CAT TTG GTT TTG AAT TAT GGT GTC							1938
Met Met Ser Gln Leu Ser His Lys His Leu Val Leu Asn Tyr Gly Val							
		600		605		610	
TGT GTC TGT GGA GAG GAG AAC ATT CTG GTT CAA GAA TTT GTA AAA TTT							1986
Cys Val Cys Gly Glu Glu Asn Ile Leu Val Gln Glu Phe Val Lys Phe							
		620		625		630	
GGA TCA CTG GAT ACA TAC CTG AAG AAG AAC AAA AAT TCC ATA AAT ATA							2034
Gly Ser Leu Asp Thr Tyr Leu Lys Lys Asn Lys Asn Ser Ile Asn Ile							
		635		640		645	
TTA TGG AAA CTT GGA GTG GCT AAG CAG TTG GCA TGG GCC ATG CAT TTT							2082
Leu Trp Lys Leu Gly Val Ala Lys Gln Leu Ala Trp Ala Met His Phe							
		650		655		660	
CTA GAA GAA AAA TCC CTT ATT CAT GGG AAT GTG TGT GCT AAA AAT ATC							2130
Leu Glu Glu Lys Ser Leu Ile His Gly Asn Val Cys Ala Lys Asn Ile							
		665		670		675	
CTG CTT ATC AGA GAA GAA GAC AGG AGA ACG GGG AAC CCA CCT TTC ATC							2178
Leu Leu Ile Arg Glu Glu Asp Arg Arg Thr Gly Asn Pro Pro Phe Ile							
		680		685		690	
AAA CTT AGT GAT CCT GGC ATT AGC ATT ACA GTT CTA CCG AAG GAC ATT							2226
Lys Leu Ser Asp Pro Gly Ile Ser Ile Thr Val Leu Pro Lys Asp Ile							
		700		705		710	
CTT CAG GAG AGA ATA CCA TGG GTA CCT CCT GAA TGC ATT GAG AAT CCT							2274
Leu Gln Glu Arg Ile Pro Trp Val Pro Pro Glu Cys Ile Glu Asn Pro							
		715		720		725	
AAA AAT CTC AAT CTG GCA ACA GAC AAG TGG AGC TTC GGG ACC ACT CTG							2322
Lys Asn Leu Asn Leu Ala Thr Asp Lys Trp Ser Phe Gly Thr Thr Leu							
		730		735		740	
TGG GAG ATC TGC AGT GGA GGA GAT AAG CCC CTG AGT GCT CTG GAT TCT							2370
Trp Glu Ile Cys Ser Gly Gly Asp Lys Pro Leu Ser Ala Leu Asp Ser							
		745		750		755	
CAA AGA AAG CTG CAG TTC TAT GAA GAT AAG CAT CAG CTT CCT GCA CCC							2418
Gln Arg Lys Leu Gln Phe Tyr Glu Asp Lys His Gln Leu Pro Ala Pro							
		760		765		770	
						775	

AAG TGG ACA GAG TTA GCA AAC CTT ATA AAT AAT TGC ATG GAC TAT GAG Lys Trp Thr Glu Leu Ala Asn Leu Ile Asn Asn Cys Met Asp Tyr Glu 780 785 790	2466
CCA GAT TTC AGG CCT GCT TTC AGA GCT GTC ATC CGT GAT CTT AAC AGC Pro Asp Phe Arg Pro Ala Phe Arg Ala Val Ile Arg Asp Leu Asn Ser 795 800 805	2514
CTG TTT ACT CCA GAT TAT GAA CTA CTA ACA GAA AAT GAC ATG CTA CCA Leu Phe Thr Pro Asp Tyr Glu Leu Leu Thr Glu Asn Asp Met Leu Pro 810 815 820	2562
AAC ATG AGA ATA GGT GCC CTA GGG TTT TCT GGT GCT TTT GAA GAC AGG Asn Met Arg Ile Gly Ala Leu Gly Phe Ser Gly Ala Phe Glu Asp Arg 825 830 835	2610
GAC CCT ACA CAG TTT GAA GAG AGA CAC TTG AAG TTT CTA CAG CAG CTT Asp Pro Thr Gln Phe Glu Glu Arg His Leu Lys Phe Leu Gln Gln Leu 840 845 850 855	2658
GGC AAA GGT AAC TTC GGG AGT GTG GAG ATG TGC CGC TAT GAC CCG CTG Gly Lys Gly Asn Phe Gly Ser Val Glu Met Cys Arg Tyr Asp Pro Leu 860 865 870	2706
CAG GAC AAC ACT GGC GAG GTG GTC GCT GTG AAG AAA CTC CAG CAC AGC Gln Asp Asn Thr Gly Glu Val Val Ala Val Lys Lys Leu Gln His Ser 875 880 885	2754
ACT GAA GAG CAC CTC CGA GAC TTT GAG AGG GAG ATC GAG ATC CTG AAA Thr Glu Glu His Leu Arg Asp Phe Glu Arg Glu Ile Glu Ile Leu Lys 890 895 900	2802
TCC TTG CAG CAT GAC AAC ATC GTC AAG TAC AAG GGA GTG TGC TAC AGT Ser Leu Gln His Asp Asn Ile Val Lys Tyr Lys Gly Val Cys Tyr Ser 905 910 915	2850
GCG GGT CGG CGC AAC CTA AGA TTA ATT ATG GAA TAT TTA CCA TAT GGA Ala Gly Arg Arg Asn Leu Arg Leu Ile Met Glu Tyr Leu Pro Tyr Gly 920 925 930 935	2898
AGT TTA CGA GAC TAT CTC CAA AAA CAT AAA GAA CGG ATA GAT CAC AAA Ser Leu Arg Asp Tyr Leu Gln Lys His Lys Glu Arg Ile Asp His Lys 940 945 950	2946
AAA CTT CTT CAA TAC ACA TCT CAG ATA TGC AAG GGC ATG GAA TAT CTT Lys Leu Leu Gln Tyr Thr Ser Gln Ile Cys Lys Gly Met Glu Tyr Leu 955 960 965	2994
GGT ACA AAA AGG TAT ATC CAC AGG GAC CTG GCA ACA AGG AAC ATA TTG Gly Thr Lys Arg Tyr Ile His Arg Asp Leu Ala Thr Arg Asn Ile Leu 970 975 980	3042
GTG GAA AAT GAG AAC AGG GTT AAA ATA GGA GAC TTC GGA TTA ACC AAA Val Glu Asn Glu Asn Arg Val Lys Ile Gly Asp Phe Gly Leu Thr Lys 985 990 995	3090
GTC TTG CCG CAG GAC AAA GAA TAC TAC AAA GTA AAG GAG CCA GGG GAA Val Leu Pro Gln Asp Lys Glu Tyr Tyr Lys Val Lys Glu Pro Gly Glu 1000 1005 1010 1015	3138
AGC CCC ATA TTC TGG TAC GCA CCT GAA TCC TTG ACG GAG AGC AAG TTT Ser Pro Ile Phe Trp Tyr Ala Pro Glu Ser Leu Thr Glu Ser Lys Phe	3186

1020										1025					1030					
TCT	GTG	GCC	TCA	GAT	GTG	TGG	AGC	TTT	GGA	GTG	GTT	CTA	TAC	GAA	CTT		3234			
Ser	Val	Ala	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Val	Leu	Tyr	Glu	Leu					
			1035					1040					1045							
TTC	ACA	TAC	ATC	GAG	AAG	AGT	AAA	AGT	CCA	CCC	GTG	GAA	TTT	ATG	CGA		3282			
Phe	Thr	Tyr	Ile	Glu	Lys	Ser	Lys	Ser	Pro	Pro	Val	Glu	Phe	Met	Arg					
		1050					1055					1060								
ATG	ATT	GGC	AAT	GAT	AAA	CAA	GGG	CAA	ATG	ATT	GTG	TTC	CAT	TTG	ATA		3330			
Met	Ile	Gly	Asn	Asp	Lys	Gln	Gly	Gln	Met	Ile	Val	Phe	His	Leu	Ile					
	1065					1070					1075									
GAG	CTA	CTG	AAG	AGC	AAC	GGA	AGA	TTG	CCA	AGG	CCA	GAA	GGA	TGC	CCA		3378			
Glu	Leu	Leu	Lys	Ser	Asn	Gly	Arg	Leu	Pro	Arg	Pro	Glu	Gly	Cys	Pro					
1080					1085				1090					1095						
GAT	GAG	ATT	TAT	GTG	ATC	ATG	ACA	GAG	TGC	TGG	AAC	AAC	AAT	GTG	AGC		3426			
Asp	Glu	Ile	Tyr	Val	Ile	Met	Thr	Glu	Cys	Trp	Asn	Asn	Asn	Val	Ser					
			1100					1105					1110							
CAG	CGT	CCC	TCC	TTC	AGG	GAC	CTT	TCG	TTC	GGG	TGG	ATC	AAA	TCC	GGG		3474			
Gln	Arg	Pro	Ser	Phe	Arg	Asp	Leu	Ser	Phe	Gly	Trp	Ile	Lys	Ser	Gly					
			1115				1120						1125							
ACA	GTA	TAGCTGCGTG	AAAGAGATGG	CCTTCACTCA	GAGACCAAGC	AGACTTCCAG											3530			
Thr	Val																			
AACCAGAACA	AAGCTCTGTA	GCCTTGTGTC	TACACATCCT	TATCATGATG	CTAGCTAGGC												3590			
AGAAGAAACT	GTGACGCCGT	CTGCTCAAAG	CTTTGCTTC														3629			

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Gly	Met	Ala	Cys	Leu	Thr	Met	Thr	Glu	Met	Glu	Ala	Thr	Ser	Thr
1				5					10					15	
Ser	Pro	Val	His	Gln	Asn	Gly	Asp	Ile	Pro	Gly	Ser	Ala	Asn	Ser	Val
			20					25					30		
Lys	Gln	Ile	Glu	Pro	Val	Leu	Gln	Val	Tyr	Leu	Tyr	His	Ser	Leu	Gly
		35					40					45			
Gln	Ala	Glu	Gly	Glu	Tyr	Leu	Lys	Phe	Pro	Ser	Gly	Glu	Tyr	Val	Ala
	50					55					60				
Glu	Glu	Ile	Cys	Val	Ala	Ala	Ser	Lys	Ala	Cys	Gly	Ile	Thr	Pro	Val
65					70					75				80	
Tyr	His	Asn	Met	Phe	Ala	Leu	Met	Ser	Glu	Thr	Glu	Arg	Ile	Trp	Tyr
			85					90						95	

Pro	Pro	Asn	His	Val	Phe	His	Ile	Asp	Glu	Ser	Thr	Arg	His	Asp	Ile	100	105	110
Leu	Tyr	Arg	Ile	Arg	Phe	Tyr	Phe	Pro	His	Trp	Tyr	Cys	Ser	Gly	Ser	115	120	125
Ser	Arg	Thr	Tyr	Arg	Tyr	Gly	Val	Ser	Arg	Gly	Ala	Glu	Ala	Pro	Leu	130	135	140
Leu	Asp	Asp	Phe	Val	Met	Ser	Tyr	Leu	Phe	Ala	Gln	Trp	Arg	His	Asp	145	150	155
Phe	Val	His	Gly	Trp	Ile	Lys	Val	Pro	Val	Thr	His	Glu	Thr	Gln	Glu	165	170	175
Glu	Cys	Leu	Gly	Met	Ala	Val	Leu	Asp	Met	Met	Arg	Ile	Ala	Lys	Glu	180	185	190
Lys	Asp	Gln	Thr	Pro	Leu	Ala	Val	Tyr	Asn	Ser	Val	Ser	Tyr	Lys	Thr	195	200	205
Phe	Leu	Pro	Lys	Cys	Val	Arg	Ala	Lys	Ile	Gln	Asp	Tyr	His	Ile	Leu	210	215	220
Thr	Arg	Lys	Arg	Ile	Arg	Tyr	Arg	Phe	Arg	Arg	Phe	Ile	Gln	Gln	Phe	225	230	235
Ser	Gln	Cys	Lys	Ala	Thr	Ala	Arg	Asn	Leu	Lys	Leu	Lys	Tyr	Leu	Ile	245	250	255
Asn	Leu	Glu	Thr	Leu	Gln	Ser	Ala	Phe	Tyr	Thr	Glu	Gln	Phe	Glu	Val	260	265	270
Lys	Glu	Ser	Ala	Arg	Gly	Pro	Ser	Gly	Glu	Glu	Ile	Phe	Ala	Thr	Ile	275	280	285
Ile	Ile	Thr	Gly	Asn	Gly	Gly	Ile	Gln	Trp	Ser	Arg	Gly	Lys	His	Lys	290	295	300
Glu	Ser	Glu	Thr	Leu	Thr	Glu	Gln	Asp	Val	Gln	Leu	Tyr	Cys	Asp	Phe	305	310	315
Pro	Asp	Ile	Ile	Asp	Val	Ser	Ile	Lys	Gln	Ala	Asn	Gln	Glu	Cys	Ser	325	330	335
Asn	Glu	Ser	Arg	Ile	Val	Thr	Val	His	Lys	Gln	Asp	Gly	Lys	Val	Leu	340	345	350
Glu	Ile	Glu	Leu	Ser	Ser	Leu	Lys	Glu	Ala	Leu	Ser	Phe	Val	Ser	Leu	355	360	365
Ile	Asp	Gly	Tyr	Tyr	Arg	Leu	Thr	Ala	Asp	Ala	His	His	Tyr	Leu	Cys	370	375	380
Lys	Glu	Val	Ala	Pro	Pro	Ala	Val	Leu	Glu	Asn	Ile	His	Ser	Asn	Cys	385	390	395
His	Gly	Pro	Ile	Ser	Met	Asp	Phe	Ala	Ile	Ser	Lys	Leu	Lys	Lys	Ala	405	410	415
Gly	Asn	Gln	Thr	Gly	Leu	Tyr	Val	Leu	Arg	Cys	Ser	Pro	Lys	Asp	Phe	420	425	430

Asn Lys Tyr Phe Leu Thr Phe Ala Val Glu Arg Glu Asn Val Ile Glu
 435 440 445
 Tyr Lys His Cys Leu Ile Thr Lys Asn Glu Asn Gly Glu Tyr Asn Leu
 450 455 460
 Ser Gly Thr Lys Arg Asn Phe Ser Asn Leu Lys Asp Leu Leu Asn Cys
 465 470 475 480
 Tyr Gln Met Glu Thr Val Arg Ser Asp Ser Ile Ile Phe Gln Phe Thr
 485 490 495
 Lys Cys Cys Pro Pro Lys Pro Lys Asp Lys Ser Asn Leu Leu Val Phe
 500 505 510
 Arg Thr Asn Gly Ile Ser Asp Val Gln Ile Ser Pro Thr Leu Gln Arg
 515 520 525
 His Asn Asn Val Asn Gln Met Val Phe His Lys Ile Arg Asn Glu Asp
 530 535 540
 Leu Ile Phe Asn Glu Ser Leu Gly Gln Gly Thr Phe Thr Lys Ile Phe
 545 550 555 560
 Lys Gly Val Arg Arg Glu Val Gly Asp Tyr Gly Gln Leu His Lys Thr
 565 570 575
 Glu Val Leu Leu Lys Val Leu Asp Lys Ala His Arg Asn Tyr Ser Glu
 580 585 590
 Ser Phe Phe Glu Ala Ala Ser Met Met Ser Gln Leu Ser His Lys His
 595 600 605
 Leu Val Leu Asn Tyr Gly Val Cys Val Cys Gly Glu Glu Asn Ile Leu
 610 615 620
 Val Gln Glu Phe Val Lys Phe Gly Ser Leu Asp Thr Tyr Leu Lys Lys
 625 630 635 640
 Asn Lys Asn Ser Ile Asn Ile Leu Trp Lys Leu Gly Val Ala Lys Gln
 645 650 655
 Leu Ala Trp Ala Met His Phe Leu Glu Glu Lys Ser Leu Ile His Gly
 660 665 670
 Asn Val Cys Ala Lys Asn Ile Leu Leu Ile Arg Glu Glu Asp Arg Arg
 675 680 685
 Thr Gly Asn Pro Pro Phe Ile Lys Leu Ser Asp Pro Gly Ile Ser Ile
 690 695 700
 Thr Val Leu Pro Lys Asp Ile Leu Gln Glu Arg Ile Pro Trp Val Pro
 705 710 715 720
 Pro Glu Cys Ile Glu Asn Pro Lys Asn Leu Asn Leu Ala Thr Asp Lys
 725 730 735
 Trp Ser Phe Gly Thr Thr Leu Trp Glu Ile Cys Ser Gly Gly Asp Lys
 740 745 750
 Pro Leu Ser Ala Leu Asp Ser Gln Arg Lys Leu Gln Phe Tyr Glu Asp
 755 760 765

Lys His Gln Leu Pro Ala Pro Lys Trp Thr Glu Leu Ala Asn Leu Ile
 770 775 780
 Asn Asn Cys Met Asp Tyr Glu Pro Asp Phe Arg Pro Ala Phe Arg Ala
 785 790 795 800
 Val Ile Arg Asp Leu Asn Ser Leu Phe Thr Pro Asp Tyr Glu Leu Leu
 805 810 815
 Thr Glu Asn Asp Met Leu Pro Asn Met Arg Ile Gly Ala Leu Gly Phe
 820 825 830
 Ser Gly Ala Phe Glu Asp Arg Asp Pro Thr Gln Phe Glu Glu Arg His
 835 840 845
 Leu Lys Phe Leu Gln Gln Leu Gly Lys Gly Asn Phe Gly Ser Val Glu
 850 855 860
 Met Cys Arg Tyr Asp Pro Leu Gln Asp Asn Thr Gly Glu Val Val Ala
 865 870 875 880
 Val Lys Lys Leu Gln His Ser Thr Glu Glu His Leu Arg Asp Phe Glu
 885 890 895
 Arg Glu Ile Glu Ile Leu Lys Ser Leu Gln His Asp Asn Ile Val Lys
 900 905 910
 Tyr Lys Gly Val Cys Tyr Ser Ala Gly Arg Arg Asn Leu Arg Leu Ile
 915 920 925
 Met Glu Tyr Leu Pro Tyr Gly Ser Leu Arg Asp Tyr Leu Gln Lys His
 930 935 940
 Lys Glu Arg Ile Asp His Lys Lys Leu Leu Gln Tyr Thr Ser Gln Ile
 945 950 955 960
 Cys Lys Gly Met Glu Tyr Leu Gly Thr Lys Arg Tyr Ile His Arg Asp
 965 970 975
 Leu Ala Thr Arg Asn Ile Leu Val Glu Asn Glu Asn Arg Val Lys Ile
 980 985 990
 Gly Asp Phe Gly Leu Thr Lys Val Leu Pro Gln Asp Lys Glu Tyr Tyr
 995 1000 1005
 Lys Val Lys Glu Pro Gly Glu Ser Pro Ile Phe Trp Tyr Ala Pro Glu
 1010 1015 1020
 Ser Leu Thr Glu Ser Lys Phe Ser Val Ala Ser Asp Val Trp Ser Phe
 1025 1030 1035 1040
 Gly Val Val Leu Tyr Glu Leu Phe Thr Tyr Ile Glu Lys Ser Lys Ser
 1045 1050 1055
 Pro Pro Val Glu Phe Met Arg Met Ile Gly Asn Asp Lys Gln Gly Gln
 1060 1065 1070
 Met Ile Val Phe His Leu Ile Glu Leu Leu Lys Ser Asn Gly Arg Leu
 1075 1080 1085
 Pro Arg Pro Glu Gly Cys Pro Asp Glu Ile Tyr Val Ile Met Thr Glu
 1090 1095 1100

Cys Trp Asn Asn Asn Val Ser Gln Arg Pro Ser Phe Arg Asp Leu Ser
1105 1110 1115 1120

Phe Gly Trp Ile Lys Ser Gly Thr Val
1125

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GCT TTC TGT GCT AAA ATG AGG AGC TCC AAG AAG ACT GAG GTG AAC	48
Met Ala Phe Cys Ala Lys Met Arg Ser Ser Lys Lys Thr Glu Val Asn	
1 5 10 15	
CTG GAG GCC CCT GAG CCA GGG GTG GAA GTG ATC TTC TAT CTG TCG GAC	96
Leu Glu Ala Pro Glu Pro Gly Val Glu Val Ile Phe Tyr Leu Ser Asp	
20 25 30	
AGG GAG CCC CTC CGG CTG GGC AGT GGA GAG TAC ACA GCA GAG GAA CTG	144
Arg Glu Pro Leu Arg Leu Gly Ser Gly Glu Tyr Thr Ala Glu Glu Leu	
35 40 45	
TGC ATC AGG GCT GCA CAG GCA TGC CGT ATC TCT CCT CTT TGT CAC AAC	192
Cys Ile Arg Ala Ala Gln Ala Cys Arg Ile Ser Pro Leu Cys His Asn	
50 55 60	
CTC TTT GCC CTG TAT GAC GAG AAC ACC AAG CTC TGG TAT GCT CCA AAT	240
Leu Phe Ala Leu Tyr Asp Glu Asn Thr Lys Leu Trp Tyr Ala Pro Asn	
65 70 75 80	
CGC ACC ATC ACC GTT GAT GAC AAG ATG TCC CTC CGG CTC CAC TAC CGG	288
Arg Thr Ile Thr Val Asp Asp Lys Met Ser Leu Arg Leu His Tyr Arg	
85 90 95	
ATG AGG TTC TAT TTC ACC AAT TGG CAT GGA ACC AAC GAC AAT GAG CAG	336
Met Arg Phe Tyr Phe Thr Asn Trp His Gly Thr Asn Asp Asn Glu Gln	
100 105 110	
TCA GTG TGG CGT CAT TCT CCA AAG AAG CAG AAA AAT GGC TAC GAG AAA	384
Ser Val Trp Arg His Ser Pro Lys Lys Gln Lys Asn Gly Tyr Glu Lys	
115 120 125	
AAA AAG ATT CCA GAT GCA ACC CCT CTC CTT GAT GCC AGC TCA CTG GAG	432
Lys Lys Ile Pro Asp Ala Thr Pro Leu Leu Asp Ala Ser Ser Leu Glu	
130 135 140	
TAT CTG TTT GCT CAG GGA CAG TAT GAT TTG GTG AAA TGC CTG GCT CCT	480
Tyr Leu Phe Ala Gln Gly Gln Tyr Asp Leu Val Lys Cys Leu Ala Pro	
145 150 155 160	

ATT CGA GAC CCC AAG ACC GAG CAG GAT GGA CAT GAT ATT GAG AAC GAG Ile Arg Asp Pro Lys Thr Glu Gln Asp Gly His Asp Ile Glu Asn Glu 165 170 175	528
TGT CTA GGG ATG GCT GTC CTG GCC ATC TCA CAC TAT GCC ATG ATG AAG Cys Leu Gly Met Ala Val Leu Ala Ile Ser His Tyr Ala Met Met Lys 180 185 190	576
AAG ATG CAG TTG CCA GAA CTG CCC AAG GAC ATC AGC TAC AAG CGA TAT Lys Met Gln Leu Pro Glu Leu Pro Lys Asp Ile Ser Tyr Lys Arg Tyr 195 200 205	624
ATT CCA GAA ACA TTG AAT AAG TCC ATC AGA CAG AGG AAC CTT CTC ACC Ile Pro Glu Thr Leu Asn Lys Ser Ile Arg Gln Arg Asn Leu Leu Thr 210 215 220	672
AGG ATG CGG ATA AAT AAT GTT TTC AAG GAT TTC CTA AAG GAA TTT AAC Arg Met Arg Ile Asn Asn Val Phe Lys Asp Phe Leu Lys Glu Phe Asn 225 230 235 240	720
AAC AAG ACC ATT TGT GAC AGC AGC GTG TCC ACG CAT GAC CTG AAG GTG Asn Lys Thr Ile Cys Asp Ser Ser Val Ser Thr His Asp Leu Lys Val 245 250 255	768
AAA TAC TTG GCT ACC TTG GAA ACT TTG ACA AAA CAT TAC GGT GCT GAA Lys Tyr Leu Ala Thr Leu Glu Thr Leu Thr Lys His Tyr Gly Ala Glu 260 265 270	816
ATA TTT GAG ACT TCC ATG TTA CTG ATT TCA TCA GAA AAT GAG ATG AAT Ile Phe Glu Thr Ser Met Leu Leu Ile Ser Ser Glu Asn Glu Met Asn 275 280 285	864
TGG TTT CAT TCG AAT GAC GGT GGA AAC GTT CTC TAC TAC GAA GTG ATG Trp Phe His Ser Asn Asp Gly Glu Asn Val Leu Tyr Tyr Glu Val Met 290 295 300	912
GTG ACT GGG AAT CTT GGA ATC CAG TGG AGG CAT AAA CCA AAT GTT GTT Val Thr Gly Asn Leu Gly Ile Gln Trp Arg His Lys Pro Asn Val Val 305 310 315 320	960
TCT GTT GAA AAG GAA AAA AAT AAA CTG AAG CGG AAA AAA CTG GAA AAT Ser Val Glu Lys Glu Lys Asn Lys Leu Lys Arg Lys Lys Leu Glu Asn 325 330 335	1008
AAA GAC AAG AAG GAT GAG GAG AAA AAC AAG ATC CGG GAA GAG TGG AAC Lys Asp Lys Lys Asp Glu Glu Lys Asn Lys Ile Arg Glu Glu Trp Asn 340 345 350	1056
AAT TTT TCA TTC TTC CCT GAA ATC ACT CAC ATT GTA ATA AAG GAG TCT Asn Phe Ser Phe Phe Pro Glu Ile Thr His Ile Val Ile Lys Glu Ser 355 360 365	1104
GTG GTC AGC ATT AAC AAG CAG GAC AAC AAG AAA ATG GAA CTG AAG CTC Val Val Ser Ile Asn Lys Gln Asp Asn Lys Lys Met Glu Leu Lys Leu 370 375 380	1152
TCT TCC CAC GAG GAG GCC TTG TCC TTT GTG TCC CTG GTA GAT GGC TAC Ser Ser His Glu Glu Ala Leu Ser Phe Val Ser Leu Val Asp Gly Tyr 385 390 395 400	1200
TTC CGG CTC ACA GCA GAT GCC CAT CAT TAC CTC TGC ACC GAC GTG GCC Phe Arg Leu Thr Ala Asp Ala His His Tyr Leu Cys Thr Asp Val Ala	1248

405	410	415	
CCC CCG TTG ATC GTC CAC AAC ATA CAG AAT GGC TGT CAT GGT CCA ATC Pro Pro Leu Ile Val His Asn Ile Gln Asn Gly Cys His Gly Pro Ile 420 425 430			1296
TGT ACA GAA TAC GCC ATC AAT AAA TTG CGG CAA GAA GGA AGC GAG GAG Cys Thr Glu Tyr Ala Ile Asn Lys Leu Arg Gln Glu Gly Ser Glu Glu 435 440 445			1344
GGG ATG TAC GTG CTG AGG TGG AGC TGC ACC GAC TTT GAC AAC ATC CTC Gly Met Tyr Val Leu Arg Trp Ser Cys Thr Asp Phe Asp Asn Ile Leu 450 455 460			1392
ATG ACC GTC ACC TGC TTT GAG AAG TCT GAG CAG GTG CAG GGT GCC CAG Met Thr Val Thr Cys Phe Glu Lys Ser Glu Gln Val Gln Gly Ala Gln 465 470 475 480			1440
AAG CAG TTC AAG AAC TTT CAG ATC GAG GTG CAG AAG GGC CGC TAC AGT Lys Gln Phe Lys Asn Phe Gln Ile Glu Val Gln Lys Gly Arg Tyr Ser 485 490 495			1488
CTG CAC GGT TCG GAC CGC AGC TTC CCC AGC TTG GGA GAC CTC ATG AGC Leu His Gly Ser Asp Arg Ser Phe Pro Ser Leu Gly Asp Leu Met Ser 500 505 510			1536
CAC CTC AAG AAG CAG ATC CTG CGC ACG GAT AAC ATC AGC TTC ATG CTA His Leu Lys Lys Gln Ile Leu Arg Thr Asp Asn Ile Ser Phe Met Leu 515 520 525			1584
AAA CGC TGC TGC CAG CCC AAG CCC CGA GAA ATC TCC AAC CTG CTG GTG Lys Arg Cys Cys Gln Pro Lys Pro Arg Glu Ile Ser Asn Leu Leu Val 530 535 540			1632
GCT ACT AAG AAA GCC CAG GAG TGG CAG CCC GTC TAC CCC ATG AGC CAG Ala Thr Lys Lys Ala Gln Glu Trp Gln Pro Val Tyr Pro Met Ser Gln 545 550 555 560			1680
CTG AGT TTC GAT CGG ATC CTC AAG AAG GAT CTG GTG CAG GGC GAG CAC Leu Ser Phe Asp Arg Ile Leu Lys Lys Asp Leu Val Gln Gly Glu His 565 570 575			1728
CTT GGG AGA GGC ACG AGA ACA CAC ATC TAT TCT GGG ACC CTG ATG GAT Leu Gly Arg Gly Thr Arg Thr His Ile Tyr Ser Gly Thr Leu Met Asp 580 585 590			1776
TAC AAG GAT GAC GAA GGA ACT TCT GAA GAG AAG AAG ATA AAA GTG ATC Tyr Lys Asp Asp Glu Gly Thr Ser Glu Glu Lys Lys Ile Lys Val Ile 595 600 605			1824
CTC AAA GTC TTA GAC CCC AGC CAC AGG GAT ATT TCC CTG GCC TTC TTC Leu Lys Val Leu Asp Pro Ser His Arg Asp Ile Ser Leu Ala Phe Phe 610 615 620			1872
GAG GCA GCC AGC ATG ATG AGA CAG GTC TCC CAC AAA CAC ATC GTG TAC Glu Ala Ala Ser Met Met Arg Gln Val Ser His Lys His Ile Val Tyr 625 630 635 640			1920
CTC TAT GGC GTC TGT GTC CGC GAC GTG GAG AAT ATC ATG GTG GAA GAG Leu Tyr Gly Val Cys Val Arg Asp Val Glu Asn Ile Met Val Glu Glu 645 650 655			1968

TTT GTG GAA GGG GGT CCT CTG GAT CTC TTC ATG CAC CGG AAA AGT GAT Phe Val Glu Gly Gly Pro Leu Asp Leu Phe Met His Arg Lys Ser Asp 660 665 670	2016
GTC CTT ACC ACA CCA TGG AAA TTC AAA GTT GCC AAA CAG CTG GCC AGT Val Leu Thr Thr Pro Trp Lys Phe Lys Val Ala Lys Gln Leu Ala Ser 675 680 685	2064
GCC CTG AGC TAC TTG GAG GAT AAA GAC CTG GTC CAT GGA AAT GTG TGT Ala Leu Ser Tyr Leu Glu Asp Lys Asp Leu Val His Gly Asn Val Cys 690 695 700	2112
ACT AAA AAC CTC CTC CTG GCC CGT GAG GGA ATC GAC AGT GAG TGT GGC Thr Lys Asn Leu Leu Leu Ala Arg Glu Gly Ile Asp Ser Glu Cys Gly 705 710 715 720	2160
CCA TTC ATC AAG CTC AGT GAC CCC GGC ATC CCC ATT ACG GTG CTG TCT Pro Phe Ile Lys Leu Ser Asp Pro Gly Ile Pro Ile Thr Val Leu Ser 725 730 735	2208
AGG CAA GAA TGC ATT GAA CGA ATC CCA TGG ATT GCT CCT GAG TGT GTT Arg Gln Glu Cys Ile Glu Arg Ile Pro Trp Ile Ala Pro Glu Cys Val 740 745 750	2256
GAG GAC TCC AAG AAC CTG AGT GTG GCT GCT GAC AAG TGG AGC TTT GGA Glu Asp Ser Lys Asn Leu Ser Val Ala Ala Asp Lys Trp Ser Phe Gly 755 760 765	2304
ACC ACG CTC TGG GAA ATC TGC TAC AAT GGC GAG ATC CCC TTG AAA GAC Thr Thr Leu Trp Glu Ile Cys Tyr Asn Gly Glu Ile Pro Leu Lys Asp 770 775 780	2352
AAG ACG CTG ATT GAG AAA GAG AGA TTC TAT GAA AGC CGG TGC AGG CCA Lys Thr Leu Ile Glu Lys Glu Arg Phe Tyr Glu Ser Arg Cys Arg Pro 785 790 795 800	2400
GTG ACA CCA TCA TGT AAG GAG CTG GCT GAC CTC ATG ACC CGC TGC ATG Val Thr Pro Ser Cys Lys Glu Leu Ala Asp Leu Met Thr Arg Cys Met 805 810 815	2448
AAC TAT GAC CCC AAT CAG AGG CCT TTC TTC CGA GCC ATC ATG AGA GAC Asn Tyr Asp Pro Asn Gln Arg Pro Phe Phe Arg Ala Ile Met Arg Asp 820 825 830	2496
ATT AAT AAG CTT GAA GAG CAG AAT CCA GAT ATT GTT TCC AGA AAA AAA Ile Asn Lys Leu Glu Glu Gln Asn Pro Asp Ile Val Ser Arg Lys Lys 835 840 845	2544
AAC CAG CCA ACT GAA GTG GAC CCC ACA CAT TTT GAG AAG CGC TTC CTA Asn Gln Pro Thr Glu Val Asp Pro Thr His Phe Glu Lys Arg Phe Leu 850 855 860	2592
AAG AGG ATC CGT GAC TTG GGA GAG GGC CAC TTT GGG AAG GTT GAG CTC Lys Arg Ile Arg Asp Leu Gly Glu Gly His Phe Gly Lys Val Glu Leu 865 870 875 880	2640
TGC AGG TAT GAC CCC GAA GAC AAT ACA GGG GAG CAG GTG GCT GTT AAA Cys Arg Tyr Asp Pro Glu Asp Asn Thr Gly Glu Gln Val Ala Val Lys 885 890 895	2688
TCT CTG AAG CCT GAG AGT GGA GGT AAC CAC ATA GCT GAT CTG AAA AAG	2736

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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Met Ala Phe Cys Ala Lys Met Arg Ser Ser Lys Lys Thr Glu Val Asn
 1             5             10             15
Leu Glu Ala Pro Glu Pro Gly Val Glu Val Ile Phe Tyr Leu Ser Asp
          20             25             30
Arg Glu Pro Leu Arg Leu Gly Ser Gly Glu Tyr Thr Ala Glu Glu Leu
          35             40             45
Cys Ile Arg Ala Ala Gln Ala Cys Arg Ile Ser Pro Leu Cys His Asn
          50             55             60
Leu Phe Ala Leu Tyr Asp Glu Asn Thr Lys Leu Trp Tyr Ala Pro Asn
          65             70             75             80
Arg Thr Ile Thr Val Asp Asp Lys Met Ser Leu Arg Leu His Tyr Arg
          85             90             95
Met Arg Phe Tyr Phe Thr Asn Trp His Gly Thr Asn Asp Asn Glu Gln
          100            105            110
Ser Val Trp Arg His Ser Pro Lys Lys Gln Lys Asn Gly Tyr Glu Lys
          115            120            125
Lys Lys Ile Pro Asp Ala Thr Pro Leu Leu Asp Ala Ser Ser Leu Glu
          130            135            140
Tyr Leu Phe Ala Gln Gly Gln Tyr Asp Leu Val Lys Cys Leu Ala Pro
          145            150            155            160
Ile Arg Asp Pro Lys Thr Glu Gln Asp Gly His Asp Ile Glu Asn Glu
          165            170            175
Cys Leu Gly Met Ala Val Leu Ala Ile Ser His Tyr Ala Met Met Lys
          180            185            190
Lys Met Gln Leu Pro Glu Leu Pro Lys Asp Ile Ser Tyr Lys Arg Tyr
          195            200            205
Ile Pro Glu Thr Leu Asn Lys Ser Ile Arg Gln Arg Asn Leu Leu Thr
          210            215            220
Arg Met Arg Ile Asn Asn Val Phe Lys Asp Phe Leu Lys Glu Phe Asn
          225            230            235            240
Asn Lys Thr Ile Cys Asp Ser Ser Val Ser Thr His Asp Leu Lys Val
          245            250            255
Lys Tyr Leu Ala Thr Leu Glu Thr Leu Thr Lys His Tyr Gly Ala Glu
          260            265            270

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Ile Phe Glu Thr Ser Met Leu Leu Ile Ser Ser Glu Asn Glu Met Asn
275 280 285

Trp Phe His Ser Asn Asp Gly Gly Asn Val Leu Tyr Tyr Glu Val Met
290 295 300

Val Thr Gly Asn Leu Gly Ile Gln Trp Arg His Lys Pro Asn Val Val
305 310 315 320

Ser Val Glu Lys Glu Lys Asn Lys Leu Lys Arg Lys Lys Leu Glu Asn
325 330 335

Lys Asp Lys Lys Asp Glu Glu Lys Asn Lys Ile Arg Glu Glu Trp Asn
340 345 350

Asn Phe Ser Phe Phe Pro Glu Ile Thr His Ile Val Ile Lys Glu Ser
355 360 365

Val Val Ser Ile Asn Lys Gln Asp Asn Lys Lys Met Glu Leu Lys Leu
370 375 380

Ser Ser His Glu Glu Ala Leu Ser Phe Val Ser Leu Val Asp Gly Tyr
385 390 395 400

Phe Arg Leu Thr Ala Asp Ala His His Tyr Leu Cys Thr Asp Val Ala
405 410 415

Pro Pro Leu Ile Val His Asn Ile Gln Asn Gly Cys His Gly Pro Ile
420 425 430

Cys Thr Glu Tyr Ala Ile Asn Lys Leu Arg Gln Glu Gly Ser Glu Glu
435 440 445

Gly Met Tyr Val Leu Arg Trp Ser Cys Thr Asp Phe Asp Asn Ile Leu
450 455 460

Met Thr Val Thr Cys Phe Glu Lys Ser Glu Gln Val Gln Gly Ala Gln
465 470 475 480

Lys Gln Phe Lys Asn Phe Gln Ile Glu Val Gln Lys Gly Arg Tyr Ser
485 490 495

Leu His Gly Ser Asp Arg Ser Phe Pro Ser Leu Gly Asp Leu Met Ser
500 505 510

His Leu Lys Lys Gln Ile Leu Arg Thr Asp Asn Ile Ser Phe Met Leu
515 520 525

Lys Arg Cys Cys Gln Pro Lys Pro Arg Glu Ile Ser Asn Leu Leu Val
530 535 540

Ala Thr Lys Lys Ala Gln Glu Trp Gln Pro Val Tyr Pro Met Ser Gln
545 550 555 560

Leu Ser Phe Asp Arg Ile Leu Lys Lys Asp Leu Val Gln Gly Glu His
565 570 575

Leu Gly Arg Gly Thr Arg Thr His Ile Tyr Ser Gly Thr Leu Met Asp
580 585 590

Tyr Lys Asp Asp Glu Gly Thr Ser Glu Glu Lys Lys Ile Lys Val Ile
595 600 605

Leu	Lys	Val	Leu	Asp	Pro	Ser	His	Arg	Asp	Ile	Ser	Leu	Ala	Phe	Phe		
610						615					620						
Glu	Ala	Ala	Ser	Met	Met	Arg	Gln	Val	Ser	His	Lys	His	Ile	Val	Tyr		
625					630					635					640		
Leu	Tyr	Gly	Val	Cys	Val	Arg	Asp	Val	Glu	Asn	Ile	Met	Val	Glu	Glu		
				645					650					655			
Phe	Val	Glu	Gly	Gly	Pro	Leu	Asp	Leu	Phe	Met	His	Arg	Lys	Ser	Asp		
			660					665					670				
Val	Leu	Thr	Thr	Pro	Trp	Lys	Phe	Lys	Val	Ala	Lys	Gln	Leu	Ala	Ser		
		675					680					685					
Ala	Leu	Ser	Tyr	Leu	Glu	Asp	Lys	Asp	Leu	Val	His	Gly	Asn	Val	Cys		
690						695					700						
Thr	Lys	Asn	Leu	Leu	Leu	Ala	Arg	Glu	Gly	Ile	Asp	Ser	Glu	Cys	Gly		
705					710					715				720			
Pro	Phe	Ile	Lys	Leu	Ser	Asp	Pro	Gly	Ile	Pro	Ile	Thr	Val	Leu	Ser		
				725					730					735			
Arg	Gln	Glu	Cys	Ile	Glu	Arg	Ile	Pro	Trp	Ile	Ala	Pro	Glu	Cys	Val		
			740					745					750				
Glu	Asp	Ser	Lys	Asn	Leu	Ser	Val	Ala	Ala	Asp	Lys	Trp	Ser	Phe	Gly		
		755					760					765					
Thr	Thr	Leu	Trp	Glu	Ile	Cys	Tyr	Asn	Gly	Glu	Ile	Pro	Leu	Lys	Asp		
		770				775					780						
Lys	Thr	Leu	Ile	Glu	Lys	Glu	Arg	Phe	Tyr	Glu	Ser	Arg	Cys	Arg	Pro		
785					790					795					800		
Val	Thr	Pro	Ser	Cys	Lys	Glu	Leu	Ala	Asp	Leu	Met	Thr	Arg	Cys	Met		
				805					810					815			
Asn	Tyr	Asp	Pro	Asn	Gln	Arg	Pro	Phe	Phe	Arg	Ala	Ile	Met	Arg	Asp		
			820					825					830				
Ile	Asn	Lys	Leu	Glu	Glu	Gln	Asn	Pro	Asp	Ile	Val	Ser	Arg	Lys	Lys		
		835					840					845					
Asn	Gln	Pro	Thr	Glu	Val	Asp	Pro	Thr	His	Phe	Glu	Lys	Arg	Phe	Leu		
		850				855					860						
Lys	Arg	Ile	Arg	Asp	Leu	Gly	Glu	Gly	His	Phe	Gly	Lys	Val	Glu	Leu		
865					870					875					880		
Cys	Arg	Tyr	Asp	Pro	Glu	Asp	Asn	Thr	Gly	Glu	Gln	Val	Ala	Val	Lys		
				885					890					895			
Ser	Leu	Lys	Pro	Glu	Ser	Gly	Gly	Asn	His	Ile	Ala	Asp	Leu	Lys	Lys		
			900					905					910				
Glu	Ile	Glu	Ile	Leu	Arg	Asn	Leu	Tyr	His	Glu	Asn	Ile	Val	Lys	Tyr		
		915					920					925					
Lys	Gly	Ile	Cys	Thr	Glu	Asp	Gly	Gly	Asn	Gly	Ile	Lys	Leu	Ile	Met		
	930					935					940						

Glu Phe Leu Pro Ser Gly Ser Leu Lys Glu Tyr Leu Pro Lys Asn Lys
 945 950 955 960

Asn Lys Ile Asn Leu Lys Gln Gln Leu Lys Tyr Ala Val Gln Ile Cys
 965 970 975

Lys Gly Met Asp Tyr Leu Gly Ser Arg Gln Tyr Val His Arg Asp Leu
 980 985 990

Ala Ala Arg Asn Val Leu Val Glu Ser Glu His Gln Val Lys Ile Gly
 995 1000 1005

Asp Phe Gly Leu Thr Lys Ala Ile Glu Thr Asp Lys Glu Tyr Tyr Thr
 1010 1015 1020

Val Lys Asp Asp Arg Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys
 1025 1030 1035 1040

Leu Met Gln Ser Lys Phe Tyr Ile Ala Ser Asp Val Trp Ser Phe Gly
 1045 1050 1055

Val Thr Leu His Glu Leu Leu Thr Tyr Cys Asp Ser Asp Ser Ser Pro
 1060 1065 1070

Met Ala Leu Phe Leu Lys Met Ile Gly Pro Thr His Gly Gln Met Thr
 1075 1080 1085

Val Thr Arg Leu Val Asn Thr Leu Lys Glu Gly Lys Arg Leu Pro Cys
 1090 1095 1100

Pro Pro Asn Cys Pro Asp Glu Val Tyr Gln Leu Met Arg Lys Cys Trp
 1105 1110 1115 1120

Glu Phe Gln Pro Ser Asn Arg Thr Ser Phe Gln Asn Leu Ile Glu Gly
 1125 1130 1135

Phe Glu Ala Leu Leu Lys
 1140

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG CCT CTG CGC CAC TGG GGG ATG GCC AGG GGC AGT AAG CCC GTT GGG	48
Met Pro Leu Arg His Trp Gly Met Ala Arg Gly Ser Lys Pro Val Gly	
1 5 10 15	
GAT GGA GCC CAG CCC ATG GCT GCC ATG GGA GGC CTG AAG GTG CTT CTG	96
Asp Gly Ala Gln Pro Met Ala Ala Met Gly Gly Leu Lys Val Leu Leu	
20 25 30	

CAC TGG GCT GGT CCA GGC GGC GGG GAG CCC TGG GTC ACT TTC AGT GAG His Trp Ala Gly Pro Gly Gly Gly Glu Pro Trp Val Thr Phe Ser Glu 35 40 45	144
TCA TCG CTG ACA GCT GAG GAA GTC TGC ATC CAC ATT GCA CAT AAA GTT Ser Ser Leu Thr Ala Glu Glu Val Cys Ile His Ile Ala His Lys Val 50 55 60	192
GGT ATC ACT CCT CCT TGC TTC AAT CTC TTT GCC CTC TTC GAT GCT CAG Gly Ile Thr Pro Pro Cys Phe Asn Leu Phe Ala Leu Phe Asp Ala Gln 65 70 75 80	240
GCC CAA GTC TGG TTG CCC CCA AAC CAC ATC CTA GAG ATC CCC AGA GAT Ala Gln Val Trp Leu Pro Pro Asn His Ile Leu Glu Ile Pro Arg Asp 85 90 95	288
GCA AGC CTG ATG CTA TAT TTC CGC ATA AGG TTT TAT TTC CGG AAC TGG Ala Ser Leu Met Leu Tyr Phe Arg Ile Arg Phe Tyr Phe Arg Asn Trp 100 105 110	336
CAT GGC ATG AAT CCT CGG GAA CCG GCT GTG TAC CGT TGT GGG CCC CCA His Gly Met Asn Pro Arg Glu Pro Ala Val Tyr Arg Cys Gly Pro Pro 115 120 125	384
GGA ACC GAG GCA TCC TCA GAT CAG ACA GCA CAG GGG ATG CAA CTC CTG Gly Thr Glu Ala Ser Ser Asp Gln Thr Ala Gln Gly Met Gln Leu Leu 130 135 140	432
GAC CCA GCC TCA TTT GAG TAC CTC TTT GAG CAG GGC AAG CAT GAG TTT Asp Pro Ala Ser Phe Glu Tyr Leu Phe Glu Gln Gly Lys His Glu Phe 145 150 155 160	480
GTG AAT GAC GTG GCA TCA CTG TGG GAG CTG TCG ACC GAG GAG GAG ATC Val Asn Asp Val Ala Ser Leu Trp Glu Leu Ser Thr Glu Glu Glu Ile 165 170 175	528
CAC CAC TTT AAG AAT GAG AGC CTG GGC ATG GCC TTT CTG CAC CTC TGT His His Phe Lys Asn Glu Ser Leu Gly Met Ala Phe Leu His Leu Cys 180 185 190	576
CAC CTC GCT CTC CGC CAT GGC ATC CCC CTG GAG GAG GTG GCC AAG AAG His Leu Ala Leu Arg His Gly Ile Pro Leu Glu Glu Val Ala Lys Lys 195 200 205	624
ACC AGC TTC AAG GAC TGC ATC CCG CGC TCC TTC CGC CGG CAT ATC CGG Thr Ser Phe Lys Asp Cys Ile Pro Arg Ser Phe Arg Arg His Ile Arg 210 215 220	672
CAG CAC AGC GCC CTG ACC CGG CTG CGC CTT CGG AAC GTC TTC CGC AGG Gln His Ser Ala Leu Thr Arg Leu Arg Leu Arg Asn Val Phe Arg Arg 225 230 235 240	720
TTC CTG CGG GAC TTC CAG CCG GGC CGA CTC TCC CAG CAG ATG GTC ATG Phe Leu Arg Asp Phe Gln Pro Gly Arg Leu Ser Gln Gln Met Val Met 245 250 255	768
GTC AAA TAC CTA GCC ACA CTC GAG CGG CTG GCA CCC CGC TTC GGC ACA Val Lys Tyr Leu Ala Thr Leu Glu Arg Leu Ala Pro Arg Phe Gly Thr 260 265 270	816
GAG CGT GTG CCC GTG TGC CAC CTG AGG CTG CTG GCC CAG GCC GAG GGG Glu Arg Val Pro Val Cys His Leu Arg Leu Leu Ala Gln Ala Glu Gly 270	864

275		280		285	
GAG CCC TGC TAC ATC CGG GAC AGT GGG GTG GCC CCT ACA GAC CCT GGC					912
Glu Pro Cys Tyr Ile Arg Asp Ser Gly Val Ala Pro Thr Asp Pro Gly					
290		295		300	
CCT GAG TCT GCT GCT GGG CCC CCA ACC CAC GAG GTG CTG GTG ACA GGC					960
Pro Glu Ser Ala Ala Gly Pro Pro Thr His Glu Val Leu Val Thr Gly					
305		310		315	320
ACT GGT GGC ATC CAG TGG TGG CCA GTA GAG GAG GAG GTG AAC AAG GAG					1008
Thr Gly Gly Ile Gln Trp Trp Pro Val Glu Glu Glu Val Asn Lys Glu					
		325		330	335
GAG GGT TCT AGT GGC AGC AGT GGC AGG AAC CCC CAA GCC AGC CTG TTT					1056
Glu Gly Ser Ser Gly Ser Ser Gly Arg Asn Pro Gln Ala Ser Leu Phe					
		340		345	350
GGG AAG AAG GCC AAG GCT CAC AAG GCA TTC GGC CAG CCG GCA GAC AGG					1104
Gly Lys Lys Ala Lys Ala His Lys Ala Phe Gly Gln Pro Ala Asp Arg					
		355		360	365
CCG CGG GAG CCA CTG TGG GCC TAC TTC TGT GAC TTC CGG GAC ATC ACC					1152
Pro Arg Glu Pro Leu Trp Ala Tyr Phe Cys Asp Phe Arg Asp Ile Thr					
		370		375	380
CAC GTG GTG CTG AAA GAG CAC TGT GTC AGC ATC CAC CGG CAG GAC AAC					1200
His Val Val Leu Lys Glu His Cys Val Ser Ile His Arg Gln Asp Asn					
		385		390	400
AAG TGC CTG GAG CTG AGC TTG CCT TCC CGG GCT GCG GCG CTG TCC TTC					1248
Lys Cys Leu Glu Leu Ser Leu Pro Ser Arg Ala Ala Ala Leu Ser Phe					
		405		410	415
GTG TCG CTG GTG GAC GGC TAT TTC CGC CTG ACG GCC GAC TCC AGC CAC					1296
Val Ser Leu Val Asp Gly Tyr Phe Arg Leu Thr Ala Asp Ser Ser His					
		420		425	430
TAC CTG TGC CAC GAG GTG GCT CCC CCA CGG CTG GTG ATG AGC ATC CGG					1344
Tyr Leu Cys His Glu Val Ala Pro Pro Arg Leu Val Met Ser Ile Arg					
		435		440	445
GAT GGG ATC CAC GGA CCC CTG CTG GAG CCA TTT GTG CAG GCC AAG CTG					1392
Asp Gly Ile His Gly Pro Leu Leu Glu Pro Phe Val Gln Ala Lys Leu					
		450		455	460
CGG CCC GAG GAC GGC CTG TAC CTC ATT CAC TGG AGC ACC AGC CAC CCC					1440
Arg Pro Glu Asp Gly Leu Tyr Leu Ile His Trp Ser Thr Ser His Pro					
		465		470	475
TAC CGC CTG ATC CTC ACA GTG GCC CAG CGT AGC CAG GCA CCA GAC GGC					1488
Tyr Arg Leu Ile Leu Thr Val Ala Gln Arg Ser Gln Ala Pro Asp Gly					
		485		490	495
ATG CAG AGC TTG CGG CTC CGA AAG TTC CCC ATT GAG CAG CAG GAC GGC					1536
Met Gln Ser Leu Arg Leu Arg Lys Phe Pro Ile Glu Gln Gln Asp Gly					
		500		505	510
GCC TTC GTG CTG GAG GGC TGG GGC CGG TCC TTC CCC AGC GTT CGG GAA					1584
Ala Phe Val Leu Glu Gly Trp Gly Arg Ser Phe Pro Ser Val Arg Glu					
		515		520	525

CTT GGG GCT GCC TTG CAG GGC TGC TTG CTG AGG GCC GGG GAT GAC TGC Leu Gly Ala Ala Leu Gln Gly Cys Leu Leu Arg Ala Gly Asp Asp Cys 530 535 540	1632
TTC TCT CTG CGT CGC TGT TGC CTG CCC CAA CCA GGA GAA ACC TCC AAT Phe Ser Leu Arg Arg Cys Cys Leu Pro Gln Pro Gly Glu Thr Ser Asn 545 550 555 560	1680
CTC ATC ATC ATG CGG GGG GCT CGG GCC AGC CCC AGG ACA CTC AAC CTC Leu Ile Ile Met Arg Gly Ala Arg Ala Ser Pro Arg Thr Leu Asn Leu 565 570 575	1728
AGC CAG CTC AGC TTC CAC CGG GTT GAC CAG AAG GAG ATC ACC CAG CTG Ser Gln Leu Ser Phe His Arg Val Asp Gln Lys Glu Ile Thr Gln Leu 580 585 590	1776
TCC CAC TTG GGC CAG GGC ACA AGG ACC AAC GTG TAT GAG GGC CGC CTG Ser His Leu Gly Gln Gly Thr Arg Thr Asn Val Tyr Glu Gly Arg Leu 595 600 605	1824
CGA GTG GAG GGC AGC GGG GAC CCT GAG GAG GGC AAG ATG GAT GAC GAG Arg Val Glu Gly Ser Gly Asp Pro Glu Glu Gly Lys Met Asp Asp Glu 610 615 620	1872
GAC CCC CTC GTG CCT GGC AGG GAC CGT GGG CAG GAG CTA CGA GTG GTG Asp Pro Leu Val Pro Gly Arg Asp Arg Gly Gln Glu Leu Arg Val Val 625 630 635 640	1920
CTC AAA GTG CTG GAC CCT AGT CAC CAT GAC ATC GCC CTG GCC TTC TAC Leu Lys Val Leu Asp Pro Ser His His Asp Ile Ala Leu Ala Phe Tyr 645 650 655	1968
GAG ACA GCC AGC CTC ATG AGC CAG GTC TCC CAC ACG CAC CTG GCC TTC Glu Thr Ala Ser Leu Met Ser Gln Val Ser His Thr His Leu Ala Phe 660 665 670	2016
GTG CAT GGC GTC TGT GTG CGC GGC CCT GAA AAT AGC ATG GTG ACA GAG Val His Gly Val Cys Val Arg Gly Pro Glu Asn Ser Met Val Thr Glu 675 680 685	2064
TAC GTG GAG CAC GGA CCC CTG GAT GTG TGG CTG CGG AGG GAG CGG GGC Tyr Val Glu His Gly Pro Leu Asp Val Trp Leu Arg Arg Glu Arg Gly 690 695 700	2112
CAT GTG CCC ATG GCT TGG AAG ATG GTG GTG GCC CAG CAG CTG GCC AGC His Val Pro Met Ala Trp Lys Met Val Val Ala Gln Gln Leu Ala Ser 705 710 715 720	2160
GCC CTC AGC TAC CTG GAG AAC AAG AAC CTG GTT CAT GGT AAT GTG TGT Ala Leu Ser Tyr Leu Glu Asn Lys Asn Leu Val His Gly Asn Val Cys 725 730 735	2208
GGC CGG AAC ATC CTG CTG GCC CGG CTG GGG TTG GCA GAG GGC ACC AGC Gly Arg Asn Ile Leu Leu Ala Arg Leu Gly Leu Ala Glu Gly Thr Ser 740 745 750	2256
CCC TTC ATC AAG CTG AGT GAT CCT GGC GTG GGC CTG GGC GCC CTC TCC Pro Phe Ile Lys Leu Ser Asp Pro Gly Val Gly Leu Gly Ala Leu Ser 755 760 765	2304
AGG GAG GAG CGG GTG GAG AGG ATC CCC TGG CTG GCC CCC GAA TGC CTA Arg Glu Glu Arg Val Glu Arg Ile Pro Trp Leu Ala Pro Glu Cys Leu	2352

770	775	780	
CCA GGT GGG GCC AAC AGC CTA AGC ACC GCC ATG GAC AAG TGG GGG TTT Pro Gly Gly Ala Asn Ser Leu Ser Thr Ala Met Asp Lys Trp Gly Phe 785 790 795 800			2400
GGC GCC ACC CTC CTG GAG ATC TGC TTT GAC GGA GAG GCC CCT CTG CAG Gly Ala Thr Leu Leu Glu Ile Cys Phe Asp Gly Glu Ala Pro Leu Gln 805 810 815			2448
AGC CGC AGT CCC TCC GAG AAG GAG CAT TTC TAC CAG AGG CAG CAC CGG Ser Arg Ser Pro Ser Glu Lys Glu His Phe Tyr Gln Arg Gln His Arg 820 825 830			2496
CTG CCC GAG CCC TCC TGC CCA CAG CTG GCC ACA CTC ACC AGC CAG TGT Leu Pro Glu Pro Ser Cys Pro Gln Leu Ala Thr Leu Ser Gln Cys 835 840 845			2544
CTG ACC TAT GAG CCA ACC CAG AGG CCA TCA TTC CGC ACC ATC CTG CGT Leu Thr Tyr Glu Pro Thr Gln Arg Pro Ser Phe Arg Thr Ile Leu Arg 850 855 860			2592
GAC CTC ACC CGC GTG CAG CCC CAC AAT CTT GCT GAC GTC TTG ACT GTG Asp Leu Thr Arg Val Gln Pro His Asn Leu Ala Asp Val Leu Thr Val 865 870 875 880			2640
AAC CGG GAC TCA CCG GCC GTC GGA CCT ACT ACT TTC CAC AAG CGC TAT Asn Arg Asp Ser Pro Ala Val Gly Pro Thr Thr Phe His Lys Arg Tyr 885 890 895			2688
TTG AAA AAG ATC CGA GAT CTG GGC GAG GGT CAC TTC GGC AAG GTC AGC Leu Lys Lys Ile Arg Asp Leu Gly Glu Gly His Phe Gly Lys Val Ser 900 905 910			2736
TTG TAC TGC TAC GAT CCG ACC AAC GAC GGC ACT GGC GAG ATG GTG GCG Leu Tyr Cys Tyr Asp Pro Thr Asn Asp Gly Thr Gly Glu Met Val Ala 915 920 925			2784
GTG AAA GCC CTC AAG GCA GAC TGC GGC CCC CAG CAC CGC TCG GGC TGG Val Lys Ala Leu Lys Ala Asp Cys Gly Pro Gln His Arg Ser Gly Trp 930 935 940			2832
AAG CAG GAG ATT GAC ATT CTG CGC ACG CTC TAC CAC GAG CAC ATC ATC Lys Gln Glu Ile Asp Ile Leu Arg Thr Leu Tyr His Glu His Ile Ile 945 950 955 960			2880
AAG TAC AAG GGC TGC TGC GAG GAC CAA GGC GAG AAG TCG CTG CAG CTG Lys Tyr Lys Gly Cys Cys Glu Asp Gln Gly Glu Lys Ser Leu Gln Leu 965 970 975			2928
GTC ATG GAG TAC GTG CCC CTG GGC AGC CTC CGA GAC TAC CTG CCC CGG Val Met Glu Tyr Val Pro Leu Gly Ser Leu Arg Asp Tyr Leu Pro Arg 980 985 990			2976
CAC AGC ATC GGG CTG GCC CAG CTG CTG CTC TTC GCC CAG CAG ATC TGC His Ser Ile Gly Leu Ala Gln Leu Leu Leu Phe Ala Gln Gln Ile Cys 995 1000 1005			3024
GAG GGC ATG GCC TAT CTG CAC GCG CAC GAC TAC ATC CAC CGA GAC CTA Glu Gly Met Ala Tyr Leu His Ala His Asp Tyr Ile His Arg Asp Leu 1010 1015 1020			3072

GCC GCG CGC AAC GTG CTG CTG GAC AAC GAC AGG CTG GTC AAG ATC GGG Ala Ala Arg Asn Val Leu Leu Asp Asn Asp Arg Leu Val Lys Ile Gly 1025 1030 1035 1040	3120
GAC TTT GGC CTA GCC AAG GCC GTG CCC GAA GGC CAC GAG TAC TAC CGC Asp Phe Gly Leu Ala Lys Ala Val Pro Glu Gly His Glu Tyr Tyr Arg 1045 1050 1055	3168
GTG CGC GAG GAT GGG GAC AGC CCC GTG TTC TGG TAT GCC CCA GAG TGC Val Arg Glu Asp Gly Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys 1060 1065 1070	3216
CTG AAG GAG TAT AAG TTC TAC TAT GCG TCA GAT GTC TGG TCC TTC GGG Leu Lys Glu Tyr Lys Phe Tyr Tyr Ala Ser Asp Val Trp Ser Phe Gly 1075 1080 1085	3264
GTG ACC CTG TAT GAG CTG CTG ACG CAC TGT GAC TCC AGC CAG AGC CCC Val Thr Leu Tyr Glu Leu Leu Thr His Cys Asp Ser Ser Gln Ser Pro 1090 1095 1100	3312
CCC ACG AAA TTC CTT GAG CTC ATA GGC ATT GCT CAG GGT CAG ATG ACA Pro Thr Lys Phe Leu Glu Leu Ile Gly Ile Ala Gln Gly Gln Met Thr 1105 1110 1115 1120	3360
GTT CTG AGA CTC ACT GAG TTG CTG GAA CGA GGG GAG AGG CTG CCA CGG Val Leu Arg Leu Thr Glu Leu Leu Glu Arg Gly Glu Arg Leu Pro Arg 1125 1130 1135	3408
CCC GAC AAA TGT CCC TGT GAG GTC TAT CAT CTC ATG AAG AAC TGC TGG Pro Asp Lys Cys Pro Cys Glu Val Tyr His Leu Met Lys Asn Cys Trp 1140 1145 1150	3456
GAG ACA GAG GCG TCC TTT CGC CCA ACC TTC GAG AAC CTC ATA CCC ATT Glu Thr Glu Ala Ser Phe Arg Pro Thr Phe Glu Asn Leu Ile Pro Ile 1155 1160 1165	3504
CTG AAG ACA GTC CAT GAG AAG TAC CAA GGC CAG GCC CCT TCA GTG TTC Leu Lys Thr Val His Glu Lys Tyr Gln Gly Gln Ala Pro Ser Val Phe 1170 1175 1180	3552
AGC GTG TGC Ser Val Cys 1185	3561

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1187 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Pro	Leu	Arg	His	Trp	Gly	Met	Ala	Arg	Gly	Ser	Lys	Pro	Val	Gly
1				5				10						15	
Asp	Gly	Ala	Gln	Pro	Met	Ala	Ala	Met	Gly	Gly	Leu	Lys	Val	Leu	Leu
		20				25							30		
His	Trp	Ala	Gly	Pro	Gly	Gly	Gly	Glu	Pro	Trp	Val	Thr	Phe	Ser	Glu

35					40					45					
Ser	Ser	Leu	Thr	Ala	Glu	Glu	Val	Cys	Ile	His	Ile	Ala	His	Lys	Val
	50					55					60				
Gly	Ile	Thr	Pro	Pro	Cys	Phe	Asn	Leu	Phe	Ala	Leu	Phe	Asp	Ala	Gln
65					70					75					80
Ala	Gln	Val	Trp	Leu	Pro	Pro	Asn	His	Ile	Leu	Glu	Ile	Pro	Arg	Asp
				85					90					95	
Ala	Ser	Leu	Met	Leu	Tyr	Phe	Arg	Ile	Arg	Phe	Tyr	Phe	Arg	Asn	Trp
			100					105					110		
His	Gly	Met	Asn	Pro	Arg	Glu	Pro	Ala	Val	Tyr	Arg	Cys	Gly	Pro	Pro
		115					120					125			
Gly	Thr	Glu	Ala	Ser	Ser	Asp	Gln	Thr	Ala	Gln	Gly	Met	Gln	Leu	Leu
	130					135					140				
Asp	Pro	Ala	Ser	Phe	Glu	Tyr	Leu	Phe	Glu	Gln	Gly	Lys	His	Glu	Phe
145					150					155					160
Val	Asn	Asp	Val	Ala	Ser	Leu	Trp	Glu	Leu	Ser	Thr	Glu	Glu	Glu	Ile
				165					170					175	
His	His	Phe	Lys	Asn	Glu	Ser	Leu	Gly	Met	Ala	Phe	Leu	His	Leu	Cys
			180					185					190		
His	Leu	Ala	Leu	Arg	His	Gly	Ile	Pro	Leu	Glu	Glu	Val	Ala	Lys	Lys
		195					200					205			
Thr	Ser	Phe	Lys	Asp	Cys	Ile	Pro	Arg	Ser	Phe	Arg	Arg	His	Ile	Arg
	210					215					220				
Gln	His	Ser	Ala	Leu	Thr	Arg	Leu	Arg	Leu	Arg	Asn	Val	Phe	Arg	Arg
225					230					235					240
Phe	Leu	Arg	Asp	Phe	Gln	Pro	Gly	Arg	Leu	Ser	Gln	Gln	Met	Val	Met
				245					250					255	
Val	Lys	Tyr	Leu	Ala	Thr	Leu	Glu	Arg	Leu	Ala	Pro	Arg	Phe	Gly	Thr
			260					265					270		
Glu	Arg	Val	Pro	Val	Cys	His	Leu	Arg	Leu	Leu	Ala	Gln	Ala	Glu	Gly
		275					280					285			
Glu	Pro	Cys	Tyr	Ile	Arg	Asp	Ser	Gly	Val	Ala	Pro	Thr	Asp	Pro	Gly
	290					295					300				
Pro	Glu	Ser	Ala	Ala	Gly	Pro	Pro	Thr	His	Glu	Val	Leu	Val	Thr	Gly
305					310					315					320
Thr	Gly	Gly	Ile	Gln	Trp	Trp	Pro	Val	Glu	Glu	Glu	Val	Asn	Lys	Glu
				325					330					335	
Glu	Gly	Ser	Ser	Gly	Ser	Ser	Gly	Arg	Asn	Pro	Gln	Ala	Ser	Leu	Phe
			340					345					350		
Gly	Lys	Lys	Ala	Lys	Ala	His	Lys	Ala	Phe	Gly	Gln	Pro	Ala	Asp	Arg
		355					360					365			

Pro 370	Arg	Glu	Pro	Leu	Trp	Ala 375	Tyr	Phe	Cys	Asp	Phe 380	Arg	Asp	Ile	Thr
His 385	Val	Val	Leu	Lys	Glu 390	His	Cys	Val	Ser	Ile 395	His	Arg	Gln	Asp	Asn 400
Lys	Cys	Leu	Glu	Leu 405	Ser	Leu	Pro	Ser	Arg 410	Ala	Ala	Ala	Leu	Ser 415	Phe
Val	Ser	Leu	Val 420	Asp	Gly	Tyr	Phe	Arg 425	Leu	Thr	Ala	Asp	Ser 430	Ser	His
Tyr	Leu	Cys 435	His	Glu	Val	Ala	Pro 440	Pro	Arg	Leu	Val	Met 445	Ser	Ile	Arg
Asp	Gly 450	Ile	His	Gly	Pro	Leu 455	Leu	Glu	Pro	Phe	Val 460	Gln	Ala	Lys	Leu
Arg 465	Pro	Glu	Asp	Gly	Leu 470	Tyr	Leu	Ile	His	Trp 475	Ser	Thr	Ser	His	Pro 480
Tyr	Arg	Leu	Ile	Leu 485	Thr	Val	Ala	Gln	Arg 490	Ser	Gln	Ala	Pro	Asp 495	Gly
Met	Gln	Ser	Leu 500	Arg	Leu	Arg	Lys	Phe 505	Pro	Ile	Glu	Gln	Gln 510	Asp	Gly
Ala	Phe	Val 515	Leu	Glu	Gly	Trp	Gly 520	Arg	Ser	Phe	Pro	Ser 525	Val	Arg	Glu
Leu	Gly 530	Ala	Ala	Leu	Gln	Gly 535	Cys	Leu	Leu	Arg	Ala 540	Gly	Asp	Asp	Cys
Phe 545	Ser	Leu	Arg	Arg	Cys 550	Cys	Leu	Pro	Gln	Pro 555	Gly	Glu	Thr	Ser	Asn 560
Leu	Ile	Ile	Met	Arg 565	Gly	Ala	Arg	Ala	Ser 570	Pro	Arg	Thr	Leu	Asn 575	Leu
Ser	Gln	Leu	Ser 580	Phe	His	Arg	Val	Asp 585	Gln	Lys	Glu	Ile	Thr 590	Gln	Leu
Ser	His	Leu 595	Gly	Gln	Gly	Thr	Arg 600	Thr	Asn	Val	Tyr	Glu 605	Gly	Arg	Leu
Arg	Val 610	Glu	Gly	Ser	Gly	Asp 615	Pro	Glu	Glu	Gly	Lys 620	Met	Asp	Asp	Glu
Asp 625	Pro	Leu	Val	Pro	Gly 630	Arg	Asp	Arg	Gly	Gln 635	Glu	Leu	Arg	Val	Val 640
Leu	Lys	Val	Leu	Asp 645	Pro	Ser	His	His	Asp 650	Ile	Ala	Leu	Ala	Phe 655	Tyr
Glu	Thr	Ala	Ser 660	Leu	Met	Ser	Gln	Val 665	Ser	His	Thr	His	Leu 670	Ala	Phe
Val	His	Gly 675	Val	Cys	Val	Arg	Gly 680	Pro	Glu	Asn	Ser	Met 685	Val	Thr	Glu
Tyr	Val 690	Glu	His	Gly	Pro	Leu 695	Asp	Val	Trp	Leu	Arg 700	Arg	Glu	Arg	Gly

His Val Pro Met Ala Trp Lys Met Val Val Ala Gln Gln Leu Ala Ser
 705 710 715 720
 Ala Leu Ser Tyr Leu Glu Asn Lys Asn Leu Val His Gly Asn Val Cys
 725 730 735
 Gly Arg Asn Ile Leu Leu Ala Arg Leu Gly Leu Ala Glu Gly Thr Ser
 740 745 750
 Pro Phe Ile Lys Leu Ser Asp Pro Gly Val Gly Leu Gly Ala Leu Ser
 755 760 765
 Arg Glu Glu Arg Val Glu Arg Ile Pro Trp Leu Ala Pro Glu Cys Leu
 770 775 780
 Pro Gly Gly Ala Asn Ser Leu Ser Thr Ala Met Asp Lys Trp Gly Phe
 785 790 795 800
 Gly Ala Thr Leu Leu Glu Ile Cys Phe Asp Gly Glu Ala Pro Leu Gln
 805 810 815
 Ser Arg Ser Pro Ser Glu Lys Glu His Phe Tyr Gln Arg Gln His Arg
 820 825 830
 Leu Pro Glu Pro Ser Cys Pro Gln Leu Ala Thr Leu Thr Ser Gln Cys
 835 840 845
 Leu Thr Tyr Glu Pro Thr Gln Arg Pro Ser Phe Arg Thr Ile Leu Arg
 850 855 860
 Asp Leu Thr Arg Val Gln Pro His Asn Leu Ala Asp Val Leu Thr Val
 865 870 875 880
 Asn Arg Asp Ser Pro Ala Val Gly Pro Thr Thr Phe His Lys Arg Tyr
 885 890 895
 Leu Lys Lys Ile Arg Asp Leu Gly Glu Gly His Phe Gly Lys Val Ser
 900 905 910
 Leu Tyr Cys Tyr Asp Pro Thr Asn Asp Gly Thr Gly Glu Met Val Ala
 915 920 925
 Val Lys Ala Leu Lys Ala Asp Cys Gly Pro Gln His Arg Ser Gly Trp
 930 935 940
 Lys Gln Glu Ile Asp Ile Leu Arg Thr Leu Tyr His Glu His Ile Ile
 945 950 955 960
 Lys Tyr Lys Gly Cys Cys Glu Asp Gln Gly Glu Lys Ser Leu Gln Leu
 965 970 975
 Val Met Glu Tyr Val Pro Leu Gly Ser Leu Arg Asp Tyr Leu Pro Arg
 980 985 990
 His Ser Ile Gly Leu Ala Gln Leu Leu Leu Phe Ala Gln Gln Ile Cys
 995 1000 1005
 Glu Gly Met Ala Tyr Leu His Ala His Asp Tyr Ile His Arg Asp Leu
 1010 1015 1020
 Ala Ala Arg Asn Val Leu Leu Asp Asn Asp Arg Leu Val Lys Ile Gly

1025	1030	1035	1040
Asp Phe Gly Leu Ala Lys Ala Val Pro Glu Gly His Glu Tyr Tyr Arg	1045	1050	1055
Val Arg Glu Asp Gly Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys	1060	1065	1070
Leu Lys Glu Tyr Lys Phe Tyr Tyr Ala Ser Asp Val Trp Ser Phe Gly	1075	1080	1085
Val Thr Leu Tyr Glu Leu Leu Thr His Cys Asp Ser Ser Gln Ser Pro	1090	1095	1100
Pro Thr Lys Phe Leu Glu Leu Ile Gly Ile Ala Gln Gly Gln Met Thr	1105	1110	1115
Val Leu Arg Leu Thr Glu Leu Leu Glu Arg Gly Glu Arg Leu Pro Arg	1125	1130	1135
Pro Asp Lys Cys Pro Cys Glu Val Tyr His Leu Met Lys Asn Cys Trp	1140	1145	1150
Glu Thr Glu Ala Ser Phe Arg Pro Thr Phe Glu Asn Leu Ile Pro Ile	1155	1160	1165
Leu Lys Thr Val His Glu Lys Tyr Gln Gly Gln Ala Pro Ser Val Phe	1170	1175	1180
Ser Val Cys	1185		

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gln Tyr Leu Asn Ile Lys Glu Asp Cys Asn Ala Met Ala Phe Cys	1	5	10	15
Ala Lys Met Arg Ser Phe Lys Lys Thr Glu Val Lys Gln Val Val Pro	20	25	30	
Glu Pro Gly Val Glu Val Thr Phe Tyr Leu Ser Asp Arg Glu Pro Leu	35	40	45	
Arg Leu Gly Ser Gly Glu Tyr Thr Ala Glu Glu Leu Cys Ile Arg Ala	50	55	60	
Ala Gln Glu Cys Ser Ile Ser Pro Leu Cys His Asn Leu Phe Ala Leu	65	70	75	80

Tyr	Asp	Glu	Ser	Thr	Lys	Leu	Trp	Tyr	Ala	Pro	Asn	Arg	Ile	Ile	Thr	
				85					90					95		
Val	Asp	Asp	Lys	Thr	Ser	Leu	Arg	Leu	His	Tyr	Arg	Met	Arg	Phe	Tyr	
			100					105					110			
Phe	Thr	Asn	Trp	His	Gly	Thr	Asn	Asp	Asn	Glu	Gln	Ser	Val	Trp	Arg	
		115					120					125				
His	Ser	Pro	Lys	Lys	Gln	Lys	Asn	Gly	Tyr	Glu	Lys	Lys	Arg	Val	Pro	
	130					135					140					
Glu	Ala	Thr	Pro	Leu	Leu	Asp	Ala	Ser	Ser	Leu	Glu	Tyr	Leu	Phe	Ala	
145					150					155					160	
Gln	Gly	Gln	Tyr	Asp	Leu	Ile	Lys	Phe	Leu	Ala	Pro	Ile	Arg	Asp	Pro	
				165					170					175		
Lys	Thr	Glu	Gln	Asp	Gly	His	Asp	Ile	Glu	Asn	Glu	Cys	Leu	Gly	Met	
			180					185					190			
Ala	Val	Leu	Ala	Ile	Ser	His	Tyr	Ala	Met	Met	Lys	Lys	Met	Gln	Leu	
		195					200					205				
Pro	Glu	Leu	Pro	Lys	Asp	Ile	Ser	Tyr	Lys	Arg	Tyr	Ile	Pro	Glu	Thr	
	210					215					220					
Leu	Asn	Lys	Ser	Ile	Arg	Gln	Arg	Asn	Leu	Leu	Thr	Arg	Met	Arg	Ile	
225					230					235					240	
Asn	Asn	Val	Phe	Lys	Asp	Phe	Leu	Lys	Glu	Phe	Asn	Asn	Lys	Thr	Ile	
				245					250					255		
Cys	Asp	Ser	Ser	Val	Ser	Thr	His	Asp	Leu	Lys	Val	Lys	Tyr	Leu	Ala	
			260					265					270			
Thr	Leu	Glu	Thr	Leu	Thr	Lys	His	Tyr	Gly	Ala	Glu	Ile	Phe	Glu	Thr	
		275					280					285				
Ser	Met	Leu	Leu	Ile	Ser	Ser	Glu	Asn	Glu	Leu	Ser	Arg	Cys	His	Ser	
	290					295					300					
Asn	Asp	Ser	Gly	Asn	Val	Leu	Tyr	Glu	Val	Met	Val	Thr	Gly	Asn	Leu	
305					310					315					320	
Gly	Ile	Gln	Trp	Arg	Gln	Lys	Pro	Asn	Val	Val	Pro	Val	Glu	Lys	Glu	
				325					330					335		
Lys	Asn	Lys	Leu	Lys	Arg	Lys	Lys	Leu	Glu	Tyr	Asn	Lys	His	Lys	Lys	
			340					345					350			
Asp	Asp	Glu	Arg	Asn	Lys	Leu	Arg	Glu	Glu	Trp	Asn	Asn	Phe	Ser	Tyr	
		355					360					365				
Phe	Pro	Glu	Ile	Thr	His	Ile	Val	Ile	Lys	Glu	Ser	Val	Val	Ser	Ile	
	370					375					380					
Asn	Lys	Gln	Asp	Asn	Lys	Asn	Met	Glu	Leu	Lys	Leu	Ser	Ser	Arg	Glu	
385					390					395					400	
Glu	Ala	Leu	Ser	Phe	Val	Ser	Leu	Val	Asp	Gly	Tyr	Phe	Arg	Leu	Thr	
				405					410					415		

Ala Asp Ala His His Tyr Leu Cys Thr Asp Val Ala Pro Pro Leu Ile
420 425 430

Val His Asn Ile Gln Asn Gly Cys His Gly Pro Ile Cys Thr Glu Tyr
435 440 445

Ala Ile Asn Lys Leu Arg Gln Glu Gly Ser Glu Glu Gly Met Tyr Val
450 455 460

Leu Arg Trp Ser Cys Thr Asp Phe Asp Asn Ile Leu Met Thr Val Thr
465 470 475 480

Cys Phe Glu Lys Ser Glu Val Leu Gly Gly Gln Lys Gln Phe Lys Asn
485 490 495

Phe Gln Ile Glu Val Gln Lys Gly Arg Tyr Ser Leu His Gly Ser Met
500 505 510

Asp His Phe Pro Ser Leu Arg Asp Leu Met Asn His Leu Lys Lys Gln
515 520 525

Ile Leu Arg Thr Asp Asn Ile Ser Phe Val Leu Lys Arg Cys Cys Gln
530 535 540

Pro Lys Pro Arg Glu Ile Ser Asn Leu Leu Val Ala Thr Lys Lys Ala
545 550 555 560

Gln Glu Trp Gln Pro Val Tyr Ser Met Ser Gln Leu Ser Phe Asp Arg
565 570 575

Ile Leu Lys Lys Asp Ile Ile Gln Gly Glu His Leu Gly Arg Gly Thr
580 585 590

Arg Thr His Ile Tyr Ser Gly Thr Leu Leu Asp Tyr Lys Asp Glu Glu
595 600 605

Gly Ile Ala Glu Glu Lys Lys Ile Lys Val Ile Leu Lys Val Leu Asp
610 615 620

Pro Ser His Arg Asp Ile Ser Leu Ala Phe Phe Glu Ala Ala Ser Met
625 630 635 640

Met Arg Gln Val Ser His Lys His Ile Val Tyr Leu Tyr Gly Val Cys
645 650 655

Val Arg Asp Val Glu Asn Ile Met Val Glu Glu Phe Val Glu Gly Gly
660 665 670

Pro Leu Asp Leu Phe Met His Arg Lys Ser Asp Ala Leu Thr Thr Pro
675 680 685

Trp Lys Phe Lys Val Ala Lys Gln Leu Ala Ser Ala Leu Ser Tyr Leu
690 695 700

Glu Asp Lys Asp Leu Val His Gly Asn Val Cys Thr Lys Asn Leu Leu
705 710 715 720

Leu Ala Arg Glu Gly Ile Asp Ser Asp Ile Gly Pro Phe Ile Lys Leu
725 730 735

Ser Asp Pro Gly Ile Pro Val Ser Val Leu Thr Arg Gln Glu Cys Ile
740 745 750

Glu	Arg	Ile	Pro	Trp	Ile	Ala	Pro	Glu	Cys	Val	Glu	Asp	Ser	Lys	Asn	755	760	765
Leu	Ser	Val	Ala	Ala	Asp	Lys	Trp	Ser	Phe	Gly	Thr	Thr	Leu	Trp	Glu	770	775	780
Ile	Cys	Tyr	Asn	Gly	Glu	Ile	Pro	Leu	Lys	Asp	Lys	Thr	Leu	Ile	Glu	785	790	795
Lys	Glu	Arg	Phe	Tyr	Glu	Ser	Arg	Cys	Arg	Pro	Val	Thr	Pro	Ser	Cys	805	810	815
Lys	Glu	Leu	Ala	Asp	Leu	Met	Thr	Arg	Cys	Met	Asn	Tyr	Asp	Pro	Asn	820	825	830
Gln	Arg	Pro	Phe	Phe	Arg	Ala	Ile	Met	Arg	Asp	Ile	Asn	Lys	Leu	Glu	835	840	845
Glu	Gln	Asn	Pro	Asp	Ile	Val	Ser	Glu	Lys	Gln	Pro	Thr	Thr	Glu	Val	850	855	860
Asp	Pro	Thr	His	Phe	Glu	Lys	Arg	Phe	Leu	Lys	Arg	Ile	Arg	Asp	Leu	865	870	875
Gly	Glu	Gly	His	Phe	Gly	Lys	Val	Glu	Leu	Cys	Arg	Tyr	Asp	Pro	Glu	885	890	895
Gly	Asp	Asn	Thr	Gly	Glu	Gln	Val	Ala	Val	Lys	Ser	Leu	Lys	Pro	Glu	900	905	910
Ser	Gly	Gly	Asn	His	Ile	Ala	Asp	Leu	Lys	Lys	Glu	Ile	Glu	Ile	Leu	915	920	925
Arg	Asn	Leu	Tyr	His	Glu	Asn	Ile	Val	Lys	Tyr	Lys	Gly	Ile	Cys	Met	930	935	940
Glu	Asp	Gly	Gly	Asn	Gly	Ile	Lys	Leu	Ile	Met	Glu	Phe	Leu	Pro	Ser	945	950	955
Gly	Ser	Leu	Lys	Glu	Tyr	Leu	Pro	Lys	Asn	Lys	Asn	Lys	Ile	Asn	Leu	965	970	975
Lys	Gln	Gln	Leu	Lys	Tyr	Ala	Ile	Gln	Ile	Cys	Lys	Gly	Met	Asp	Tyr	980	985	990
Leu	Gly	Ser	Arg	Gln	Tyr	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	995	1000	1005
Leu	Val	Glu	Ser	Glu	His	Gln	Val	Lys	Ile	Gly	Asp	Phe	Gly	Leu	Thr	1010	1015	1020
Lys	Ala	Ile	Glu	Thr	Asp	Lys	Glu	Tyr	Tyr	Thr	Val	Lys	Asp	Asp	Arg	1025	1030	1035
Asp	Ser	Pro	Val	Phe	Trp	Tyr	Ala	Pro	Glu	Cys	Leu	Ile	Gln	Cys	Lys	1045	1050	1055
Phe	Tyr	Ile	Ala	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Thr	Leu	His	Glu	1060	1065	1070
Leu	Leu	Thr	Tyr	Cys	Asp	Ser	Asp	Ser	Phe	Pro	Met	Ala	Leu	Phe	Leu	1075	1080	1085

Lys Met Ile Gly Pro Thr His Gly Gln Met Thr Val Thr Arg Leu Val
 1090 1095 1100

Asn Thr Leu Lys Glu Gly Lys Arg Leu Pro Cys Pro Pro Asn Cys Pro
 1105 1110 1115 1120

Asp Glu Val Tyr Gln Leu Met Arg Lys Cys Trp Glu Phe Gln Pro Ser
 1125 1130 1135

Asn Arg Thr Thr Phe Gln Asn Leu Ile Glu Gly Phe Glu Ala Leu Leu
 1140 1145 1150

Lys

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Lys Leu Leu Pro Leu Asp Lys Asp Tyr Tyr Val Val Arg Glu Pro
 1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1099 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Pro Pro Ser Glu Glu Thr Pro Leu Ile Pro Gln Arg Ser Cys
 1 5 10 15

Ser Leu Ser Ser Ser Glu Ala Gly Ala Leu His Val Leu Leu Pro Pro
 20 25 30

Arg Gly Pro Gly Pro Pro Gln Arg Leu Ser Phe Ser Phe Gly Asp Tyr
 35 40 45

Leu Ala Glu Asp Leu Cys Val Arg Ala Ala Lys Ala Cys Gly Ile Leu
 50 55 60

Pro Val Tyr His Ser Leu Phe Ala Leu Ala Thr Glu Asp Phe Ser Cys
 65 70 75 80

Trp Phe Pro Pro Ser His Ile Phe Cys Ile Glu Asp Val Asp Thr Gln

				85				90				95			
Val	Leu	Val	Tyr 100	Arg	Leu	Arg	Phe	Tyr 105	Phe	Pro	Asp	Trp	Phe 110	Gly	Leu
Glu	Thr	Cys 115	His	Arg	Phe	Gly	Leu 120	Arg	Lys	Asp	Leu	Thr 125	Ser	Ala	Ile
Leu	Asp 130	Leu	His	Val	Leu	Glu 135	His	Leu	Phe	Ala	Gln 140	His	Arg	Ser	Asp
Leu 145	Val	Ser	Gly	Arg	Leu 150	Pro	Val	Gly	Leu	Ser 155	Met	Lys	Glu	Gln	Gly 160
Glu	Phe	Leu	Ser	Leu 165	Ala	Val	Leu	Asp	Leu 170	Ala	Gln	Met	Ala	Arg 175	Glu
Gln	Ala	Gln	Arg 180	Pro	Gly	Glu	Leu 185	Leu	Lys	Thr	Val	Ser 190	Tyr	Lys	Ala
Cys	Leu	Pro 195	Pro	Ser	Leu	Arg	Asp 200	Val	Ile	Gln	Gly 205	Gln	Asn	Phe	Val
Thr	Arg 210	Arg	Arg	Ile	Arg	Arg 215	Thr	Val	Val	Leu 220	Ala	Leu	Leu	Pro	Cys
Gly 225	Arg	Leu	Pro	Gly	Arg 230	Pro	Tyr	Ala	Leu	Met 235	Ala	Lys	Tyr	Ile	Leu 240
Asp	Leu	Glu	Arg	Leu 245	His	Pro	Ala	Ala	Thr 250	Thr	Glu	Thr	Phe	Arg 255	Val
Gly	Leu	Pro	Gly 260	Ala	Gln	Glu	Glu	Pro 265	Gly	Leu	Leu	Arg	Val 270	Ala	Gly
Asp	Asn	Gly 275	Ile	Pro	Trp	Ser	Ser 280	Asn	Asp	Glu	Leu	Phe 285	Gln	Thr	Phe
Cys	Asp 290	Phe	Pro	Glu	Ile	Val 295	Asp	Val	Ser	Ile	Asn 300	Gln	Ala	Pro	Arg
Val 305	Gly	Pro	Ala	Gly	Glu 310	His	Arg	Leu	Val	Thr 315	Val	Thr	Arg	Met	Asp 320
Gly	His	Ile	Leu	Glu 325	Ala	Glu	Phe	Pro	Gly 330	Leu	Pro	Glu	Ala	Leu 335	Ser
Phe	Val	Ala	Leu 340	Val	Asp	Gly	Tyr	Phe 345	Arg	Leu	Ile	Cys	Asp 350	Ser	Arg
His	Tyr	Phe 355	Cys	Lys	Glu	Val	Ala 360	Pro	Pro	Arg	Leu 365	Leu	Glu	Glu	Glu
Ala	Asp 370	Val	Cys	His	Gly	Pro 375	Ile	Thr	Leu	Asp	Phe 380	Ala	Ile	His	Lys
Leu 385	Lys	Ala	Ala	Gly	Ser 390	Leu	Pro	Gly	Thr	Tyr 395	Ile	Leu	Arg	Arg	Ser 400
Pro	Gln	Asp	Tyr	Asp 405	Ser	Phe	Leu	Leu	Thr 410	Ala	Cys	Val	Gln	Thr 415	Pro

Leu Gly Pro Asp Tyr Lys Gly Cys Leu Ile Arg Gln Asp Pro Ser Gly
 420 425 430
 Ala Phe Ser Leu Val Gly Leu Ser Gln Pro His Arg Ser Leu Arg Glu
 435 440 445
 Leu Leu Ala Ala Cys Trp Asn Ser Gly Leu Arg Val Asp Gly Ala Ala
 450 455 460
 Leu Tyr Leu Thr Ser Cys Cys Ala Pro Arg Pro Lys Glu Lys Ser Asn
 465 470 475 480
 Leu Ile Val Val Arg Arg Gly Cys Asn Pro Ala Pro Ala Pro Gly Cys
 485 490 495
 Ser Pro Ser Cys Cys Ala Leu Thr Gln Leu Ser Phe His Thr Ile Pro
 500 505 510
 Thr Asp Ser Leu Glu Trp His Glu Asn Leu Gly His Gly Ser Phe Thr
 515 520 525
 Lys Ile Phe Arg Gly Ser Arg Arg Glu Val Val Asp Gly Glu Thr His
 530 535 540
 Asp Ser Glu Val Leu Leu Lys Val Met Asp Ser Arg His Arg Asn Cys
 545 550 555 560
 Met Glu Ser Phe Leu Glu Ala Ala Ser Leu Met Ser Gln Val Ser Tyr
 565 570 575
 Pro His Leu Val Leu Leu His Gly Val Cys Met Ala Gly Asp Ser Ile
 580 585 590
 Met Val Gln Glu Phe Val Tyr Leu Gly Ala Ile Asp Met Tyr Leu Arg
 595 600 605
 Lys Arg Gly His Leu Val Ser Ala Ser Trp Lys Leu Gln Val Thr Lys
 610 615 620
 Gln Leu Ala Tyr Ala Leu Asn Tyr Leu Glu Asp Lys Gly Leu Pro His
 625 630 635 640
 Gly Asn Val Ser Ala Arg Lys Val Leu Leu Ala Arg Glu Gly Gly Asp
 645 650 655
 Gly Asn Pro Pro Phe Ile Lys Leu Ser Asp Pro Gly Val Ser Pro Thr
 660 665 670
 Val Leu Ser Leu Glu Met Leu Thr Asp Arg Ile Pro Trp Val Ala Pro
 675 680 685
 Glu Cys Leu Gln Glu Ala Gln Thr Leu Cys Leu Glu Ala Asp Lys Trp
 690 695 700
 Gly Phe Gly Ala Thr Thr Trp Glu Val Phe Gln Arg Gly Pro Ala His
 705 710 715 720
 Ile Thr Ser Leu Glu Pro Ala Lys Lys Leu Lys Phe Tyr Glu Asp Gln
 725 730 735
 Gly Gln Leu Pro Ala Leu Lys Trp Thr Glu Leu Ala Gly Leu Ile Thr
 740 745 750

Gln Cys Met Ala Tyr Asp Pro Gly Arg Arg Pro Ser Phe Arg Ala Ile
755 760 765

Leu Arg Asp Leu Asn Gly Leu Ile Thr Ser Asp Tyr Glu Leu Leu Ser
770 775 780

Asp Pro Thr Pro Gly Ile Pro Ser Pro Arg Asp Glu Leu Cys Val Ala
785 790 795 800

Gly Ala Gln Leu Tyr Ala Cys Gln Asp Pro Ala Ile Phe Glu Glu Arg
805 810 815

His Leu Lys Tyr Ile Ser Leu Leu Gly Lys Gly Asn Phe Gly Ser Val
820 825 830

Glu Leu Cys Arg Tyr Asp Pro Leu Gly Asp Asn Thr Gly Pro Leu Val
835 840 845

Ala Val Lys Gln Leu Gln His Ser Val Pro Asp Gln Gln Arg Asp Phe
850 855 860

Gln Arg Glu Ile Gln Ile Leu Lys Ala Leu His Ser Asp Phe Ile Val
865 870 875 880

Lys Tyr Arg Gly Val Ser Tyr Gly Pro Gly Arg Gln Ser Leu Arg Leu
885 890 895

Val Met Glu Tyr Leu Pro Ser Gly Cys Leu Arg Asp Leu Leu Gln Arg
900 905 910

His Arg Gly Leu His Thr Asp Arg Leu Leu Leu Phe Ala Trp Gln Ile
915 920 925

Cys Lys Gly Met Glu Tyr Leu Gly Ala Arg Arg Cys Val His Arg Asp
930 935 940

Leu Ala Ala Arg Asn Ile Leu Val Glu Ser Glu Ala His Val Lys Ile
945 950 955 960

Ala Asp Phe Gly Leu Ala Lys Leu Leu Pro Leu Gly Lys Asp Tyr Tyr
965 970 975

Val Val Arg Glu Pro Gly Gln Ser Pro Ile Phe Trp Tyr Ala Pro Glu
980 985 990

Ser Leu Ser Asp Asn Ile Phe Ser Arg Gln Ser Asp Val Trp Ser Phe
995 1000 1005

Gly Val Val Leu Tyr Glu Leu Phe Thr Tyr Cys Asp Lys Ser Cys Ser
1010 1015 1020

Pro Ser Ala Glu Phe Leu Arg Met Met Gly Pro Glu Arg Glu Gly Pro
1025 1030 1035 1040

Pro Leu Cys Arg Leu Leu Glu Leu Leu Ala Glu Gly Arg Arg Leu Pro
1045 1050 1055

Pro Pro Pro Thr Cys Pro Thr Glu Val Gln Glu Leu Met Gln Leu Cys
1060 1065 1070

Trp Ala Pro Glu Pro His Asp Arg Pro Ala Phe Ala Thr Leu Ser Pro
1075 1080 1085

Gln Leu Asp Pro Leu Trp Arg Gly Arg Pro Gly
1090 1095